

# Sequence Listing

<110> Ashkenazi, Avi  
 Baker Kevin P.  
 Botstein, David  
 Desnoyers, Luc  
 Eaton, Dan  
 Ferrara, Napoleon  
 Filvaroff, Ellen  
 Fong, Sherman  
 Gao, Wei-Qiang  
 Gerber, Hanspeter  
 Gerritsen, Mary E.  
 Goddard, Audrey  
 Godowski, Paul J.  
 Grimaldi, J. Christopher  
 Gurney, Austin L.  
 Hillan, Kenneth J.  
 Kljavin, Ivar J.  
 Kuo, Sophia S.  
 Napier, Mary A.  
 Pan, James;  
 Paoni, Nicholas F.  
 Roy, Margaret Ann  
 Shelton, David L.  
 Stewart, Timothy A.  
 Tumas, Daniel  
 Williams, P. Mickey  
 Wood, William I.

<120> Secreted and Transmembrane Polypeptides and Nucleic  
 Acids Encoding the Same

<130> P2630P1C66

<150> 09/918585

<151> 2001-07-30

<150> 60/062250

<151> 1997-10-17

<150> 60/064249

<151> 1997-11-03

<150> 60/065311

<151> 1997-11-13

<150> 60/066364

<151> 1997-11-21

<150> 60/077450

<151> 1998-03-10

<150> 60/077632

<151> 1998-03-11

<150> 60/077641

<151> 1998-03-11

PROJECT FOOT

<150> 60/077649  
<151> 1998-03-11

<150> 60/077791  
<151> 1998-03-12

<150> 60/078004  
<151> 1998-03-13

<150> 60/078886  
<151> 1998-03-20

<150> 60/078936  
<151> 1998-03-20

<150> 60/078910  
<151> 1998-03-20

<150> 60/078939  
<151> 1998-03-20

<150> 60/079294  
<151> 1998-03-25

<150> 60/079656  
<151> 1998-03-26

<150> 60/079664  
<151> 1998-03-27

<150> 60/079689  
<151> 1998-03-27

<150> 60/079663  
<151> 1998-03-27

<150> 60/079728  
<151> 1998-03-27

<150> 60/079786  
<151> 1998-03-27

<150> 60/079920  
<151> 1998-03-30

<150> 60/079923  
<151> 1998-03-30

<150> 60/080105  
<151> 1998-03-31

<150> 60/080107  
<151> 1998-03-31

<150> 60/080165  
<151> 1998-03-31

<150> 60/080194

1998-03-31

<151> 1998-03-31

<150> 60/080327  
<151> 1998-04-01

<150> 60/080328  
<151> 1998-04-01

<150> 60/080333  
<151> 1998-04-01

<150> 60/080334  
<151> 1998-04-01

<150> 60/081070  
<151> 1998-04-08

<150> 60/081049  
<151> 1998-04-08

<150> 60/081071  
<151> 1998-04-08

<150> 60/081195  
<151> 1998-04-08

<150> 60/081203  
<151> 1998-04-09

<150> 60/081229  
<151> 1998-04-09

<150> 60/081955  
<151> 1998-04-15

<150> 60/081817  
<151> 1998-04-15

<150> 60/081819  
<151> 1998-04-15

<150> 60/081952  
<151> 1998-04-15

<150> 60/081838  
<151> 1998-04-15

<150> 60/082568  
<151> 1998-04-21

<150> 60/082569  
<151> 1998-04-21

<150> 60/082704  
<151> 1998-04-22

<150> 60/082804  
<151> 1998-04-22

<150> 60/082700  
<151> 1998-04-22

<150> 60/082797  
<151> 1998-04-22

<150> 60/082796  
<151> 1998-04-23

<150> 60/083336  
<151> 1998-04-27

<150> 60/083322  
<151> 1998-04-28

<150> 60/083392  
<151> 1998-04-29

<150> 60/083495  
<151> 1998-04-29

<150> 60/083496  
<151> 1998-04-29

<150> 60/083499  
<151> 1998-04-29

<150> 60/083545  
<151> 1998-04-29

<150> 60/083554  
<151> 1998-04-29

<150> 60/083558  
<151> 1998-04-29

<150> 60/083559  
<151> 1998-04-29

<150> 60/083500  
<151> 1998-04-29

<150> 60/083742  
<151> 1998-04-30

<150> 60/084366  
<151> 1998-05-05

<150> 60/084414  
<151> 1998-05-06

<150> 60/084441  
<151> 1998-05-06

<150> 60/084637  
<151> 1998-05-07

<150> 60/084639

T.04237-13047007



100-430400

<151> 1998-05-07

<150> 60/084640  
<151> 1998-05-07

<150> 60/084598  
<151> 1998-05-07

<150> 60/084600  
<151> 1998-5-07

<150> 60/084627  
<151> 1998-05-07

<150> 60/084643  
<151> 1998-05-07

<150> 60/085339  
<151> 1998-05-13

<150> 60/085338  
<151> 1998-05-13

<150> 60/085323  
<151> 1998-05-13

<150> 60/085582  
<151> 1998-05-15

<150> 60/085700  
<151> 1998-05-15

<150> 60/085689  
<151> 1998-05-15

<150> 60/085579  
<151> 1998-05-15

<150> 60/085580  
<151> 1998-05-15

<150> 60/085573  
<151> 1998-05-15

<150> 60/085704  
<151> 1998-05-15

<150> 60/085697  
<151> 1998-05-15

<150> 60/086023  
<151> 1998-05-18

<150> 60/086430  
<151> 1998-05-22

<150> 60/086392  
<151> 1998-05-22

<150> 60/086486  
<151> 1998-05-22

<150> 60/086414  
<151> 1998-05-22

<150> 60/087208  
<151> 1998-05-28

<150> 60/087106  
<151> 1998-05-28

<150> 60/087098  
<151> 1998-05-28

<150> 60/091010  
<151> 1998-06-26

<150> 60/090863  
<151> 1998-06-26

<150> 60/091359  
<151> 1998-07-01

<150> 60/094651  
<151> 1998-07-30

<150> 60/100038  
<151> 1998-09-11

<150> 60/109304  
<151> 1998-11-20

<150> 60/113296  
<151> 1998-12-22

<150> 60/113621  
<151> 1998-12-23

<150> 60/123957  
<151> 1999-03-12

<150> 60/126773  
<151> 1999-03-29

<150> 60/130232  
<151> 1999-04-21

<150> 60/131022  
<151> 1999-04-26

<150> 60/131445  
<151> 1999-04-28

<150> 60/134287  
<151> 1999-05-14

<150> 60/139557

FOIA b 7 - DEDUCTIBLE

[illegible]

<150> 09/380138  
<151> 1999-08-25

<150> 09/380142  
<151> 1999-08-25

<150> 09/709238  
<151> 2000-11-08

<150> 09/723749  
<151> 2000-11-27

<150> 09/747259  
<151> 2000-12-20

<150> 09/816744  
<151> 2001-03-22

<150> 09/816920  
<151> 2001-03-22

<150> 09/854280  
<151> 2001-05-10

<150> 09/854208  
<151> 2001-05-10

<150> 09/872035  
<151> 2001-06-01

<150> 09/874503  
<151> 2001-06-05

<150> 09/882636  
<151> 2001-06-14

<150> 09/886342  
<151> 2001-06-19

<150> PCT/US98/21141  
<151> 1998-10-07

<150> PCT/US98/24855  
<151> 1998-11-20

<150> PCT/US99/00106  
<151> 1999-01-05

<150> PCT/US99/05028  
<151> 1999-03-08

<150> PCT/US99/05190  
<151> 1999-03-10

<150> PCT/US99/10733  
<151> 1999-05-14

<150> PCT/US99/12252  
<151> 1999-06-02

<150> PCT/US99/28313

FOOTNOTES

<151> 1999-11-30

<150> PCT/US99/28551

<151> 1999-12-02

<150> PCT/US99/28565

<151> 1999-12-02

<150> PCT/US99/30095

<151> 1999-12-16

<150> PCT/US99/31243

<151> 1999-12-30

<150> PCT/US99/31274

<151> 1999-12-30

<150> PCT/US00/00219

<151> 2000-05-01

<150> PCT/US00/00277

<151> 2000-01-06

<150> PCT/US00/00376

<151> 2000-01-06

<150> PCT/US00/03565

<151> 2000-02-11

<150> PCT/US00/04341

<151> 2000-02-18

<150> PCT/US00/05841

<151> 2000-03-02

<150> PCT/US00/07532

<151> 2000-03-21

<150> PCT/US00/05004

<151> 2000-02-24

<150> PCT/US00/06319

<151> 2000-03-10

<150> PCT/US00/08439

<151> 2000-03-30

<150> PCT/US00/13705

<151> 2000-05-17

<150> PCT/US00/14042

<151> 2000-05-22

<150> PCT/US00/14941

<151> 2000-05-30

<150> PCT/US00/15264

<151> 2000-06-02

TELECOM-19000000

<150> PCT/US00/20710  
 <151> 2000-07-28  
  
 <150> PCT/US00/23328  
 <151> 2000-08-24  
  
 <150> PCT/US00/32678  
 <151> 2000-12-01  
  
 <150> PCT/US00/34956  
 <151> 2000-12-20  
  
 <150> PCT/US01/06520  
 <151> 2001-02-28  
  
 <150> PCT/US01/09552  
 <151> 2001-03-22  
  
 <150> PCT/US01/17092  
 <151> 2001-05-25  
  
 <150> PCT/US01/17800  
 <151> 2001-06-01  
  
 <150> PCT/US01/19692  
 <151> 2001-06-20  
  
 <150> PCT/US01/21066  
 <151> 2001-06-29  
  
 <150> PCT/US01/21735  
 <151> 2001-07-09  
  
 <160> 624  
  
 <210> 1  
 <211> 1743  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 1  
 ccaggtccaa ctgcacctcg gttctatcga ttgaattccc cggggatcct 50  
 ctagagatcc ctgcacctcg acccacgcgt ccgccaagct ggccctgcac 100  
 ggctgcaagg gaggctcctg tggacaggcc aggcaggtgg gcctcaggag 150  
 gtgcctccag gcggccagtg ggcctgaggc cccagcaagg gctaggggtcc 200  
 atctccagtc ccaggacaca gcagcggcca ccatggccac gcctggggtc 250  
 cagcagcatc agcagccccc aggaccggg gaggcacagg tggccccac 300  
 caccggagg agcagctcct gccctgtcc gggggatgac tgattctcct 350  
 ccgccaggcc acccagagga gaaggccacc ccgcctggag gcacaggcca 400  
 tgagggggtc tcaggaggtg ctgctgatgt ggcttctggt gttggcagtg 450



Met	Thr	Asp	Ser	Pro	Pro	Pro	Gly	His	Pro	Glu	Glu	Lys	Ala	Thr	1	5	10	15
Pro	Pro	Gly	Gly	Thr	Gly	His	Glu	Gly	Leu	Ser	Gly	Gly	Ala	Ala	20	25	30	
Asp	Val	Ala	Ser	Gly	Val	Gly	Ser	Gly	Arg	His	Arg	Ala	Arg	Leu	35	40	45	
Pro	Ala	Arg	Pro	Leu	Gly	Cys	Val	Leu	Ser	Arg	Ala	His	Gly	Asp	50	55	60	
Pro	Val	Ser	Glu	Ser	Phe	Val	Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	65	70	75	
Thr	Thr	Cys	Asp	Gly	His	Arg	Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	80	85	90	
Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	95	100	105	
Pro	Arg	Tyr	Ala	Cys	Cys	Pro	Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	110	115	120	
Pro	Gly	Ala	Cys	Gly	Ala	Ala	Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	125	130	135	
Gly	Gly	Ser	Cys	Val	Gln	Pro	Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	140	145	150	
Trp	Arg	Gly	Asp	Thr	Cys	Gln	Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	155	160	165	
Arg	Arg	Gly	Gly	Cys	Pro	Gln	Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	170	175	180	
Tyr	Trp	Cys	Gln	Cys	Trp	Glu	Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	185	190	195	
Thr	Leu	Cys	Val	Pro	Lys	Gly	Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	200	205	210	
Pro	Thr	Gly	Val	Asp	Ser	Ala	Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	215	220	225	
Gln	Ser	Arg	Val	Asp	Leu	Leu	Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	230	235	240	
Ala	Pro	Leu	His	Ser	Leu	Ala	Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	245	250	255	
Pro	Asp	Pro	Gly	Ser	Leu	Leu	Val	His	Ser	Phe	Gln	Gln	Leu	Gly	260	265	270	
Arg	Ile	Asp	Ser	Leu	Ser	Glu	Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	275	280	285	
Leu	Gly	Ser	Cys	Ser	Cys	Lys	Lys	Asp	Ser									



<210> 3  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 3  
 tggagcagca atatgccagc c 21

<210> 4  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 4  
 ttttcactc ctgtcgggtt gg 22

<210> 5  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 5  
 ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 6  
 <211> 2945  
 <212> DNA  
 <213> Homo sapiens

<400> 6  
 cgctcgcccc gtgcgcccc gcctccccgc agagtccct cgcggcagca 50  
 gatgtgtgtg gggtcagccc acggcgggga ctatggtgaa attcccggcg 100  
 ctacgcact actggcccct gatccgggtt ttggtgcccc tgggcatcac 150  
 caacatagcc atcgacttcg gggagcaggc cttgaaccgg ggcattgctg 200  
 ctgtcaagga ggatgcagtc gagatgctgg ccagctacgg gctggcgtac 250  
 tccctcatga agttcttcac ggtcccatg agtgacttca aaaatgtggg 300  
 cctggtgttt gtgaacagca agagagacag gaccaaagcc gtcctgtgta 350  
 tggtggtggc aggggccatc gctgcogtct ttcacacact gatagcttat 400  
 agtgatttag gatactacat tatcaataaa ctgcaccatg tggacgagtc 450







Protein: h304T001

Pro	Asn	Val	Ser	Glu	Lys	Ile	Leu	Ile	Asp	Ile	Ile	Gly	Val	Asp
				350					355					360
Phe	Ala	Phe	Ala	Glu	Leu	Cys	Val	Val	Pro	Leu	Arg	Ile	Phe	Ser
				365					370					375
Phe	Phe	Pro	Val	Pro	Val	Thr	Val	Arg	Ala	His	Leu	Thr	Gly	Trp
				380					385					390
Leu	Met	Thr	Leu	Lys	Lys	Thr	Phe	Val	Leu	Ala	Pro	Ser	Ser	Val
				395					400					405
Leu	Arg	Ile	Ile	Val	Leu	Ile	Ala	Ser	Leu	Val	Val	Leu	Pro	Tyr
				410					415					420
Leu	Gly	Val	His	Gly	Ala	Thr	Leu	Gly	Val	Gly	Ser	Leu	Leu	Ala
				425					430					435
Gly	Phe	Val	Gly	Glu	Ser	Thr	Met	Val	Ala	Ile	Ala	Ala	Cys	Tyr
				440					445					450
Val	Tyr	Arg	Lys	Gln	Lys	Lys	Lys	Met	Glu	Asn	Glu	Ser	Ala	Thr
				455					460					465
Glu	Gly	Glu	Asp	Ser	Ala	Met	Thr	Asp	Met	Pro	Pro	Thr	Glu	Glu
				470					475					480
Val	Thr	Asp	Ile	Val	Glu	Met	Arg	Glu	Glu	Asn	Glu			
				485					490					

<210> 8  
<211> 535  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> unsure  
<222> 33, 66, 96, 387  
<223> unknown base

<400> 8  
cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50  
tgagcttctg gtgcntttg gctctaattc tggccacaca gagaancagt 100  
cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150  
agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200  
tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250  
aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300  
ggccacatc aagaagttca ccttcgtctg catggctctg tcaactcacgc 350  
tctgtttcgt gatgttttgg acaccaacg tgtctgngaa aatcttgata 400  
gacatcatcg gaggaggactt tgcctttgca gaactctgtg ttgttccttt 450

gcggatcttc tcctttctcc cagttccagt cacagtgagg gcgcattca 500

ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9

<211> 434

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273, 293, 296, 305, 336, 358, 361

<223> unknown base

<400> 9

tgacggaatc ccgggtggg tctctgggt tngacaagat aaacccccag 50

caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100

agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttcgtgat 150

gttttggaaca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200

tggantttgc ctttgcagaa ntttgnngtg ttcttttgcg gattttctcc 250

ttttcccag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350

ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400

gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10

<211> 154

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 33, 49, 68, 83, 90, 98, 119

<223> unknown base

<400> 10

tattcccagt tccggtcacg gggagggcgc atntcaccgg gtggctgang 50

acactgaaga aaaccttngt ccttgcccc agntttgtgn tgccgatnat 100

cgctcctatc gccagcctng tggctcctacc ctacctgggg gtgcacggtg 150

agac 154

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 11  
ctgatccggt tcttggtgcc cctg 24

<210> 12  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 12  
gctctgtcac tcacgctc 18

<210> 13  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 13  
tcattctctc cctctccc 18

<210> 14  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 14  
ccttcgcca cggagtgc 18

<210> 15  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 15  
ggcaaagtc actccgatga tgtc 24

<210> 16  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 16  
gcctgctgtg gtcacaggtc tccg 24

<210> 17

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 17

tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18

<211> 1901

<212> DNA

<213> Homo sapiens

<400> 18

gccccgcgcc cggcgccggg cgcccgaagc cgggagccac cgccatgggg 50

gcctgccttg gagcctgtc cctgtcagc tgcgcgtcct gcctctgcgg 100

ctctgcccc tgcctcctgt gcagctgtg ccccgccagc cgcaactcca 150

ccgtgagccg cctcatcttc acgttcttcc tcttcctggg ggtgctggtg 200

tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250

ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300

tcgactgttg ctccctgctt ggctaccgag ctgtctaccg catgtgcttc 350

gccacggcgg ccttcttctt cttctttttt accctgctca tgctctgcgt 400

gagcagcagc cgggaccccc gggctgccat ccagaatggg ttttggttct 450

ttaagttcct gatcctggtg ggcctcaccg tgggtgcctt ctacatccct 500

gacggctcct tcaccaacat ctggttctac ttcggcgtcg tgggctcctt 550

cctcttcac ctcattccagc tgggtgtgct catcgacttt gcgcactcct 600

ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg 650

tacgcaggcc tcttcttctt cactctcttc ttctacttgc tgcgatcgc 700

ggccgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750

agggcaaggt cttcatcagc ctcaacctca cttctgtgt ctgcgtgtcc 800

atcgtcgtg tctgccccaa ggtccaggac gccagccca actcgggtct 850

gctgcaggcc tcggtcatca cctctacac catgtttgtc acctggtcag 900

ccctatccag tatccctgaa cagaaatgca accccattt gccaaaccag 950

104201-180000







350	355	360
Leu Asp Ala Thr Gln Gln Gln Gln Gln Gln Val Ala Ala Cys Glu		
365	370	375
Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr		
380	385	390
Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met		
395	400	405
Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr Arg Lys Met		
410	415	420
Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp		
425	430	435
Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu		
440	445	450

Leu Arg Asn Arg Asp Phe Ser  
455

Footnote 1800000

<210> 20  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 20  
gccgcctcat cttcacgttc ttcc 24

<210> 21  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 21  
tcatccagct ggtgctgctc 20

<210> 22  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 22  
cttcttccac ttctgcctgg 20

<210> 23  
<211> 18



actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300  
 cccagagccc tattaccggg aatctggatg ggaccgcctc cgggagctgt 350  
 ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400  
 aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450  
 agcttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500  
 tttatcataa cgggtttgat gctgtgcaat ctgcacatcg tgctgccaca 550  
 cgaggcttca ttcgttatgg ctggcgctgg ggttgagaaa ctgcagtgtt 600  
 tgtgactata ttcaacacag tgaacactag tctgaatgta taccgaaata 650  
 aagatgcctt aagccatttt gtaattgcag gagctgtcac ggggaagtctt 700  
 tttaggataa acgtaggcct gcgtggcctg gtggctggtg gcataattgg 750  
 agccttgctg ggcaactcctg taggaggcct gctgatggca tttcagaagt 800  
 acgctggtga gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850  
 catgagctaa aactggaaga gtggaaaggc agactacaag ttactgagca 900  
 cctccctgag aaaattgaaa gtagtttacg ggaagatgaa cctgagaatg 950  
 atgctaagaa aattgaagca ctgctaaacc ttcctagaaa cccttcagta 1000  
 atagataaac aagacaagga ctgaaagtgc tctgaacttg aaactcactg 1050  
 gagagctgaa gggagctgcc atgtccgatg aatgccaaca gacaggccac 1100  
 tctttggtca gcctgctgac aaatttaagt gctggtacct gtggtggcag 1150  
 tggcttgctc ttgtcttttt cttttctttt taactaagaa tggggctgtt 1200  
 gtactctcac tttacttata cttaaattta aatacatact tatgtttgta 1250  
 ttaatctatc aatatatgca tacatggata tatccacca cctagatttt 1300  
 aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt 1350

t 1351

<210> 28

<211> 285

<212> PRT

<213> Homo sapiens

<400> 28

Met	Glu	Val	Pro	Pro	Pro	Ala	Pro	Arg	Ser	Phe	Leu	Cys	Arg	Ala
1				5					10					15

Leu	Cys	Leu	Phe	Pro	Arg	Val	Phe	Ala	Ala	Glu	Ala	Val	Thr	Ala
				20					25					30

Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val	35	40	45
Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu	50	55	60
Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala	65	70	75
Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val	80	85	90
Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile	95	100	105
Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val	110	115	120
Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly	125	130	135
Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	140	145	150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	155	160	165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	170	175	180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	185	190	195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	200	205	210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	215	220	225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	230	235	240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	245	250	255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	260	265	270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	275	280	285

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 29

cggaagtccc ttgaggagcg tcagaagcgg cttccctacg tcccagagcc 50

ctattacccg gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100  
 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150  
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200  
 catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250  
 ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300  
 ttcgttcattg gctggcgccg aacc 324

<210> 30  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 262, 330, 371  
 <223> unknown base

TOH2017-10-10

<400> 30  
 tcaagtttgt ccgtaggtcg agagaaggcc atggaggtgc cgccaccggc 50  
 accgcggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100  
 gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150  
 gcggcttccc tacgtccag agccctatta cccggaattt ggatgggacc 200  
 gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250  
 cttgtgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300  
 gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350  
 agagccaggc agaaatttat nataacc 377

<210> 31  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 31  
 tcgtacagtt acgctctccc 20

<210> 32  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 32  
cttgaggagc gtcagaagcg 20

<210> 33  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 33  
ataacgaatg aagcctcgtg 20

<210> 34  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 34  
gctaatatct gtaagacggc agctacagca ggcattcattg 40

<210> 35  
<211> 1819  
<212> DNA  
<213> Homo sapiens

<400> 35  
gagccgcccgc cgcgcgcgcgc cgcgcgcactg cagccccagg ccccgggccc 50  
ccaccacagt ctgcgttgct gcccgcctg ggccaggccc caaaggcaag 100  
gacaaagcag ctgtcaggga acctccgcgc gagtcgaatt tacgtgcagc 150  
tgccggcaac cacaggttcc aagatggttt gcgggggctt cgcgtgttcc 200  
aagaactgcc tgtgcgcctt caacctgctt tacaccttg ttagtctgct 250  
gctaattgga attgctgcgt ggggcattgg cttcgggctg atttccagtc 300  
tccgagtggc cggcgtggc attgcagtgg gcattcttctt gttcctgatt 350  
gctttagtgg gtctgattgg agctgtaaaa catcatcagg tgttgctatt 400  
tttttatatg attattctgt tacttgtatt tattgttcag tttctgtat 450  
cttgcgcttg tttagccctg aaccaggagc aacagggtca gcttctggag 500  
gttggttgga acaatacggc aagtgtcga aatgacatcc agagaaatct 550  
aaactgctgt gggttccgaa gtgttaaccc aatgacacc tgtctggcta 600  
gctgtgttaa aagtgaccac tcgtgctcgc catgtgctcc aatcatagga 650  
gaatatgctg gagaggtttt gagatttggt ggtggcattg gcctgttctt 700





protein-3000

Ala Ala Trp Gly Ile Gly Phe Gly Leu Ile Ser Ser Leu Arg Val  
35 40 45  
Val Gly Val Val Ile Ala Val Gly Ile Phe Leu Phe Leu Ile Ala  
50 55 60  
Leu Val Gly Leu Ile Gly Ala Val Lys His His Gln Val Leu Leu  
65 70 75  
Phe Phe Tyr Met Ile Ile Leu Leu Leu Val Phe Ile Val Gln Phe  
80 85 90  
Ser Val Ser Cys Ala Cys Leu Ala Leu Asn Gln Glu Gln Gln Gly  
95 100 105  
Gln Leu Leu Glu Val Gly Trp Asn Asn Thr Ala Ser Ala Arg Asn  
110 115 120  
Asp Ile Gln Arg Asn Leu Asn Cys Cys Gly Phe Arg Ser Val Asn  
125 130 135  
Pro Asn Asp Thr Cys Leu Ala Ser Cys Val Lys Ser Asp His Ser  
140 145 150  
Cys Ser Pro Cys Ala Pro Ile Ile Gly Glu Tyr Ala Gly Glu Val  
155 160 165  
Leu Arg Phe Val Gly Gly Ile Gly Leu Phe Phe Ser Phe Thr Glu  
170 175 180  
Ile Leu Gly Val Trp Leu Thr Tyr Arg Tyr Arg Asn Gln Lys Asp  
185 190 195  
Pro Arg Ala Asn Pro Ser Ala Phe Leu  
200

<210> 37  
<211> 390  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336  
<223> unknown base

<400> 37  
tgattggagc tgtaaaaaan tcttcaggtg ttgtnatttt ttatatgat 50  
tattctgtaa ntgtatttta ttgttcagtt ttntgtatct tgcgcttggt 100  
tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tgggtggaac 150  
aatacgcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200  
gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250  
gtgaccactn gtgctcgcca tgtgctcaa tcataggaga atatgctgga 300

gaggttttga gatttggttg tggcattggc ctgttnttca gttttacaga 350  
gatcctgggt gtttggtga cctacagata caggaaccag 390

<210> 38  
<211> 566  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 27  
<223> unknown base

<400> 38  
aatcccaaāt tccccaattt ttttgnctt tttagggaaa gatgtgtgt 50  
ggtaaaaagt gttagtataa aaatgataat ttactttag tcttttatga 100  
ttacaccaat gtattctaga atagtattgt cttaggaaat tgtggtttaa 150  
tttttgactt ttacaggtaa gtgcaaagga gaagtggttt catgaaatgt 200  
tctaattgtat aataacattt accttcagcc tcccatcaga atggaacgag 250  
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300  
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350  
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400  
ccgttttcat gaaagtctc agtattgtaa cagcaacttg tcaaacctaa 450  
gcatatttga atatgatctc ccataatttg aaattgaaat cgtattgtgt 500  
ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550  
gttgtgcccc acttgc 566

<210> 39  
<211> 264  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 84-85, 206  
<223> unknown base

<400> 39  
atgattattc tgttacttgt atttattgtt cagttttatg gtatcttgcg 50  
cttgttttagc ccctgaaacc aggagcaaca gggnnacagt tcttgagggt 100  
tggttgcaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150  
aatcctaaac tgctgtgggt tccgaagtgt taaccctaat gacacctgtc 200

tggtngctg tgttaaaagt gaccactcgt gctcgccatg tgctccaatc 250

ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40

accacgtct gcgttgctgc c 21

<210> 41

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 41

gagaatatgc tggagagg 18

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 42

aggaatgcac taggattcgc gcgg 24

<210> 43

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 43

ggccccaaag gcaaggacaa agcagctgtc agggaacctc cgccg 45

<210> 44

<211> 2061

<212> DNA

<213> Homo sapiens

<400> 44

cagtcacat gaagctgggc tgtgtcctca tggcctgggc cctctacctt 50

tcccttggtg tgctctgggt ggcccagatg ctactggctg ccagttttga 100

gacgctgcag tgtgaggagac ctgtctgcac tgaggagagc agctgccaca 150  
 cggaggatga cttgactgat gcaaggaag ctggcttcca ggtcaaggcc 200  
 tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat 250  
 cctccaaggt ccagccaagc cagtttttga aggggacctg ctggttctgc 300  
 gctgccaggc ctggcaagac tggccactga ctcaggtgac cttctaccga 350  
 gatggctcag ctctgggtcc ccccgggcct aacagggaat tctccatcac 400  
 cgtggtacaa aaggcagaca gcgggcacta cactgcagt ggcatcttcc 450  
 agagccctgg tcttgggatc ccagaaacag catctgttgt ggctatcaca 500  
 gtccaagaac tgtttccagc gccattctc agagctgtac ctcagctga 550  
 accccaagca ggaagccca tgacctgag ttgtcagaca aagttgcccc 600  
 tgcagaggtc agctgccgc ctctcttct cttctacaa ggatggaagg 650  
 atagtcaaa gcagggggct ctctcagaa ttccagatcc ccacagcttc 700  
 agaagatcac tccgggtcat actggtgtga ggcagccact gaggacaacc 750  
 aagtttgaa acagagcccc cagctagaga tcagagtga ggtgcttcc 800  
 agctctgctg cacctccac attgaatcca gtcctcaga aatcagctgc 850  
 tccaggaact gtcctgagg aggccctgg gcctctgcct ccgcccga 900  
 ccccatcttc tgaggatcca ggcttttct ctctctggg gatgccagat 950  
 cctcatctgt atcaccagat gggccttct ctcaaacaca tgcaggatgt 1000  
 gagagtcctc ctgggtcacc tgctcatgga gttgaggaa ttatctggc 1050  
 accagaagcc tgggaccaca aaggctactg ctgaatagaa gtaaacagtt 1100  
 catccatgat ctacttaac caccacaata aatctgattc tttattttct 1150  
 ctctctgtcc tgcacatatg cataagtact tttacaagtt gtcccagtg 1200  
 tttgttagaa taatgtagt aggtgagtgt aaataaattt atataaagt 1250  
 agaattagag tttagctata attgtgtatt ctctcttaac acaacagaat 1300  
 tctgctgtct agatcaggaa tttctatctg ttatatcgac cagaatgttg 1350  
 tgatttaaag agaactaatg gaagtggatt gaatacagca gtctcaactg 1400  
 ggggcaattt tgccccccag aggacattgg gcaatgttg gagacatttt 1450  
 ggtcattata cttggggggg tgggggatgg tgggatgtgt gtctactggc 1500  
 atccagtaaa tagaagccag ggtgcccgt aaacatccta taatgcacag 1550

ggagtagccc cacaacgaaa aataatctgg cccaaaatgt cagttgtact 1600  
 gagtttgaga aacccagacc taatgaaacc ctagggtgtg ggctctggaa 1650  
 tgggactttg tcccttctaa ttattatctc ttccagcct cattcagcta 1700  
 ttcttactga cataccagtc tttagctggg gctatggtct gttctttagt 1750  
 tctagtttgt atccctcaa aagccattat gttgaaatcc taatcccaa 1800  
 ggtgatggca ttaagaagtg ggcctttggg aagtgattag atcaggagtg 1850  
 cagagccctc atgattagga ttagtgcctt tatttaaaaa ggccccagag 1900  
 agctaactca cccttcacc atatgaggac gtggcaagaa gatgacatgt 1950  
 atgagaacca aaaaacagct gtcgccaac accgactctg tcgttgccct 2000  
 gatcttgaac ttccagcctc cagaactatg agaaataaaa ttctggttgt 2050  
 ttgtagccta a. 2061

<210> 45  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

<400> 45  
 Met Lys Leu Gly Cys Val Leu Met Ala Trp Ala Leu Tyr Leu Ser  
 1 5 10 15  
 Leu Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe  
 20 25 30  
 Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser  
 35 40 45  
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe  
 50 55 60  
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val  
 65 70 75  
 Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe  
 80 85 90  
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp  
 95 100 105  
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly  
 110 115 120  
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys  
 125 130 135  
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro  
 140 145 150



<220>  
<223> Synthetic oligonucleotide probe

<400> 47  
tttccagcgc caattctc 18

<210> 48  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 48  
agttcttgga ctgtgatagc cac 23

<210> 49  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 49  
aaacttggtt gtcctcagtg gctg 24

<210> 50  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 50  
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51  
<211> 2181  
<212> DNA  
<213> Homo sapiens

<400> 51  
cccacgcgtc cgcccacgcg tccgcccacg ggtccgccca cgcgtccggg 50  
ccaccagaag tttgagcctc tttggttagca ggaggctgga agaaaggaca 100  
gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150  
gcacctaaaca gtggacactt atggccgtcc catcctggaa gtgccagaga 200  
gtgtaacagg accttggaag ggggatgtga atcttccttg cacctatgac 250  
cccctgcaag gctacacca agtcttggtg aagtggctgg tacaacgtgg 300  
ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc 350



agcaggcaaa gtaccagggc cgcctgcatg tgagccacaa ggttccagga 400  
 gatgtatccc tccaattgag caccctggag atggatgacc ggagccacta 450  
 cagtggtgaa gtcacctggc agactcctga tggcaaccaa gtcgtgagag 500  
 ataagattac tgagctccgt gtccagaaac tctctgtctc caagcccaca 550  
 gtgacaactg gcagcgggta tggcttcacg gtgccccagg gaatgaggat 600  
 tagccttcaa tgccaggctc ggggttctcc tcccatcagt tatatttggg 650  
 ataagcaaca gactaataac caggaacca tcaaagtagc aaccctaagt 700  
 accttactct tcaagcctgc ggtgatagcc gactcaggct cctatttctg 750  
 cactgccaaag ggccagggtg gctctgagca gcacagcgac attgtgaagt 800  
 ttgtggtaa agactcctca aagctactca agaccaagac tgaggcacct 850  
 acaaccatga cataccccctt gaaagcaaca tctacagtga agcagtcctg 900  
 ggactggacc actgacatgg atggctacct tggagagacc agtgcctggc 950  
 caggaaagag cctgcctgtc ttgccaatca tctcatcat ctccttgtgc 1000  
 tgtatggtgg tttttaccat ggcctatatc atgctctgtc ggaagacatc 1050  
 ccaacaagag catgtctacg aagcagccag gtaagaaagt ctctcctctt 1100  
 ccatttttga ccccgctcct gccctcaatt ttgattactg gcaggaaatg 1150  
 tggaggaagg ggggtgtggc acagacccaa tcctaaggcc ggaggccttc 1200  
 agggtcagga catagctgcc ttccctctct caggcacctt ctgaggttgt 1250  
 tttggccctc tgaacacaaa ggataattta gatccatctg ccttctgctt 1300  
 ccagaatccc tgggtggtag gatcctgata attaattggc aagaattgag 1350  
 gcagaagggt gggaaaccag gaccacagcc ccaagtcctt tcttatgggt 1400  
 ggtgggctct tgggcatag ggcacatgcc agagaggcca acgactctgg 1450  
 agaaaccatg agggtgcca tcttcgcaag tggctgctcc agtgatgagc 1500  
 caacttccca gaatctgggc aacaactact ctgatgagcc ctgcatagga 1550  
 caggagtacc agatcatogc ccagatcaat ggcaactacg cccgcctgct 1600  
 ggacacagtt cctctggatt atgagtttct ggccactgag ggcaaaagt 1650  
 tctgttaaaa atgccccatt aggccaggat ctgctgacat aattgcctag 1700  
 tcagtccttg ccttctgcat ggccttcttc cctgctacct ctcttcctgg 1750  
 atagcccaaa gtgtccgcct accaactctg gagccgctgg gagtcactgg 1800

ctttgccctg gaatttgcca gatgcatctc aagtaagcca gctgctggat 1850  
 ttggctctgg gcccttctag tatctctgcc gggggcttct ggtactcctc 1900  
 tctaaatacc agagggaaga tgcccatagc actaggactt ggatcatcatg 1950  
 cctacagaca ctattcaact ttggcatctt gccaccagaa gacccgaggg 2000  
 aggctcagct ctgccagctc agaggaccag ctatatccag gatcatttct 2050  
 ctttcttcag ggccagacag cttttaattg aaattgttat ttcacaggcc 2100  
 agggttcagt tctgctcctc cactataagt ctaatgttct gactctctcc 2150  
 tgggtctcaa taaatatcta atcataacag c 2181

<210> 52

<211> 321

<212> PRT

<213> Homo sapiens

<400> 52

Met	Gly	Ile	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Gly	His	Leu	Thr	Val	1	5	10	15
Asp	Thr	Tyr	Gly	Arg	Pro	Ile	Leu	Glu	Val	Pro	Glu	Ser	Val	Thr	20	25	30	
Gly	Pro	Trp	Lys	Gly	Asp	Val	Asn	Leu	Pro	Cys	Thr	Tyr	Asp	Pro	35	40	45	
Leu	Gln	Gly	Tyr	Thr	Gln	Val	Leu	Val	Lys	Trp	Leu	Val	Gln	Arg	50	55	60	
Gly	Ser	Asp	Pro	Val	Thr	Ile	Phe	Leu	Arg	Asp	Ser	Ser	Gly	Asp	65	70	75	
His	Ile	Gln	Gln	Ala	Lys	Tyr	Gln	Gly	Arg	Leu	His	Val	Ser	His	80	85	90	
Lys	Val	Pro	Gly	Asp	Val	Ser	Leu	Gln	Leu	Ser	Thr	Leu	Glu	Met	95	100	105	
Asp	Asp	Arg	Ser	His	Tyr	Thr	Cys	Glu	Val	Thr	Trp	Gln	Thr	Pro	110	115	120	
Asp	Gly	Asn	Gln	Val	Val	Arg	Asp	Lys	Ile	Thr	Glu	Leu	Arg	Val	125	130	135	
Gln	Lys	Leu	Ser	Val	Ser	Lys	Pro	Thr	Val	Thr	Thr	Gly	Ser	Gly	140	145	150	
Tyr	Gly	Phe	Thr	Val	Pro	Gln	Gly	Met	Arg	Ile	Ser	Leu	Gln	Cys	155	160	165	
Gln	Ala	Arg	Gly	Ser	Pro	Pro	Ile	Ser	Tyr	Ile	Trp	Tyr	Lys	Gln	170	175	180	

Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr  
185 190 195

Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser Tyr Phe  
200 205 210

Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp Ile  
215 220 225

Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys  
230 235 240

Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser  
245 250 255

Thr Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr  
260 265 270

Leu Gly Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe  
275 280 285

Ala Ile Ile Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr  
290 295 300

Met Ala Tyr Ile Met Leu Cys Arg Lys Thr Ser Gln Gln Glu His  
305 310 315

Val Tyr Glu Ala Ala Arg  
320

<210> 53  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 53  
tatccctcca attgagcacc ctgg 24

<210> 54  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 54  
gtcggagac atccaacaa g 21

<210> 55  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 55

cttcacaatg tcgctgtgct gctc 24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 56

agccaaatcc agcagctggc ttac 24

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 57

tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58

<211> 2458

<212> DNA

<213> Homo sapiens

<400> 58

gcgccgggag cccatctgcc cccaggggca cggggcgcg ggccggctcc 50

cgccccgcac atggctgcag ccacctcgcg cgcaccccga ggcgcgcgc 100

ccagctcgcc cgaggtccgt cggaggcgcc cggccgcccc ggagccaagc 150

agcaactgag cggggaagcg cccgcgtccg gggatcgga tgtccctoct 200

ccttctctc ttgctagttt cctactatgt tggaaccttg gggactcaca 250

ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccacat 300

caactggggc ttccagaaaa agacactctg gatattgaat ggctgctcac 350

cgataatgaa gggaaccaa aagtgtgat cacttactcc agtcgtcatg 400

tctacaataa cttgactgag gaacagaagg gccgagtggc ctttgcttcc 450

aatttctg caggagatgc ctcttgagc attgaacctc tgaagcccag 500

tgatgagggc cggtagacct gtaagggtta gaattcagg cgctacgtgt 550

ggagccatgt catcttaaaa gtottagtga gaccatccaa gcccaagtgt 600

gagttggaag gagagctgac agaaggaagt gacctgactt tgcagtgtga 650

gtcatcctct ggcacagagc ccattgtgta ttactggcag cgaatccgag 700  
 agaaagaggg agaggatgaa cgtctgcctc ccaaactag gattgactac 750  
 aaccaccctg gacgagttct gctgcagaat cttaccatgt cctactctgg 800  
 actgtaccag tgcacagcag gcaacgaagc tgggaaggaa agctgtgtgg 850  
 tgcgagtaac tgtacagtat gtacaaagca tcggcatggg tgcaggagca 900  
 gtgacaggca tagtggctgg agccctgctg attttcctct tgggtgtggct 950  
 gctaattccga aggaaagaca aagaaagata tgaggaagaa gagagaccta 1000  
 atgaaattcg agaagatgct gaagctcaa aagcccgctt tgtgaaacct 1050  
 agctcctctt cctcaggtc tcggagctca cgtctgtggt cttcctccac 1100  
 tcgctccaca gcaaatagtg cctcacgcag ccagcggaca ctgtcaactg 1150  
 acgcagcacc ccagccaggg ctggccaccc aggcatacag cctagtgggg 1200  
 ccagaggtga gaggttctga accaaagaaa gtccaccatg ctaattctgac 1250  
 caaagcagaa accacacca gcatgatccc cagccagagc agagccttcc 1300  
 aaacggtctg aattacaatg gacttgactc ccacgcttcc ctaggagtca 1350  
 gggctcttgg actcttctcg tcattggagc tcaagtcacc agccacacaa 1400  
 ccagatgaga ggtcatctaa gtagcagtga gcattgcacg gaacagattc 1450  
 agatgagcat tttccttata caataccaaa caagcaaaag gatgtaagct 1500  
 gattcatctg taaaaaggca tcttattgtg ccttttagacc agagtaaggg 1550  
 aaagcaggag tccaaatcta tttgttgacc aggacctgtg gtgagaaggt 1600  
 tggggaaagg tgaggtgaat atacctaaa cttttaatgt gggatatttt 1650  
 gtatcagtgc ttgattcac aattttcaag aggaaatggg atgctgtttg 1700  
 taaattttct atgcatttct gcaaacttat tggattatta gttattcaga 1750  
 cagtcaagca gaaccacag cttattaca cctgtctaca ccatgtactg 1800  
 agctaaccac ttctaagaaa ctccaaaaaa ggaaacatgt gtcttctatt 1850  
 ctgacttaac ttcatttgct ataaggtttg gatattaatt tcaaggggag 1900  
 ttgaaatagt gggagatgga gaagagtga tgagtttctc ccactctata 1950  
 ctaatctcac tatttgtatt gagcccaaaa taactatgaa aggagacaaa 2000  
 aatttgtgac aaaggattgt gaagagcttt ccatcttcat gatgttatga 2050  
 ggattgttga caaacattag aaatatataa tggagcaatt gtggatttcc 2100

cctcaaatca gatgcctcta aggactttcc tgctagatat ttctggaagg 2150  
 agaaaatata acatgtcatt tatcaacgtc cctagaaaga attcttctag 2200  
 agaaaaaggg atctaggaat gctgaaagat tacccaacat accattatag 2250  
 tctcttcttt ctgagaaaat gtgaaaccag aattgcaaga ctgggtggac 2300  
 tagaaagga gattagatca gttttctctt aatatgtcaa ggaaggtagc 2350  
 cgggcatggt gccaggcacc tgtaggaaaa tccagcaggt ggaggttgca 2400  
 gtgagccgag attatgccat tgcactccag cctgggtgac agagcgggac 2450  
 tccgtctc 2458

<210> 59

<211> 373

<212> PRT

<213> Homo sapiens

<400> 59

Met	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Val	Ser	Tyr	Tyr	Val	Gly	1	5	10	15
Thr	Leu	Gly	Thr	His	Thr	Glu	Ile	Lys	Arg	Val	Ala	Glu	Glu	Lys	20	25	30	
Val	Thr	Leu	Pro	Cys	His	His	Gln	Leu	Gly	Leu	Pro	Glu	Lys	Asp	35	40	45	
Thr	Leu	Asp	Ile	Glu	Trp	Leu	Leu	Thr	Asp	Asn	Glu	Gly	Asn	Gln	50	55	60	
Lys	Val	Val	Ile	Thr	Tyr	Ser	Ser	Arg	His	Val	Tyr	Asn	Asn	Leu	65	70	75	
Thr	Glu	Glu	Gln	Lys	Gly	Arg	Val	Ala	Phe	Ala	Ser	Asn	Phe	Leu	80	85	90	
Ala	Gly	Asp	Ala	Ser	Leu	Gln	Ile	Glu	Pro	Leu	Lys	Pro	Ser	Asp	95	100	105	
Glu	Gly	Arg	Tyr	Thr	Cys	Lys	Val	Lys	Asn	Ser	Gly	Arg	Tyr	Val	110	115	120	
Trp	Ser	His	Val	Ile	Leu	Lys	Val	Leu	Val	Arg	Pro	Ser	Lys	Pro	125	130	135	
Lys	Cys	Glu	Leu	Glu	Gly	Glu	Leu	Thr	Glu	Gly	Ser	Asp	Leu	Thr	140	145	150	
Leu	Gln	Cys	Glu	Ser	Ser	Ser	Gly	Thr	Glu	Pro	Ile	Val	Tyr	Tyr	155	160	165	
Trp	Gln	Arg	Ile	Arg	Glu	Lys	Glu	Gly	Glu	Asp	Glu	Arg	Leu	Pro	170	175	180	



<400> 61  
actaggtgt atgcctgggt ggc 24

<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

gtatgtacaa agcatcggca tggttgcagg agcagtgaca ggc 43

<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

gtcgttcctt tgcctctctg cgcccagtc tcttccttg ttctcctcag 50

ccgtgtcgg aggagagcac ccggagacgc gggctgcagt cgcggcggct 100

tctccccgcc tgggcggcct cgcgctggg caggtgctga gcgcccctag 150

agcctccctt gccgcctccc tctctgccc ggccgcagca gtgcacatgg 200

ggtgttgagg gtagatggg tcccgcccc ggaggcggcg gtggatgcgg 250

cgctgggcag aagcagccgc cgattccagc tgccccgcgc gccccggcg 300

cccctgcgag tccccggttc agccatggg acctctccga gcagcagcac 350

cgccctcgcc tctgcagcc gcctgcgcc ccgagccaca gccacgatga 400

tgcggggtc ccttctctg cttggattcc ttagcaccac cacagctcag 450

ccagaacaga aggcctcgaa tctcattggc acataccgcc atgttgaccg 500

tgccaccggc caggtgctaa cctgtgacaa gtgtccagca ggaacctatg 550

tctctgagca ttgtaccaac acaagcctgc gcgtctgcag cagttgccct 600

gtggggacct ttaccaggca tgagaatggc atagagaaat gccatgactg 650

tagtcagcca tgcccatggc caatgattga gaaattacct tgtgctgcct 700

tgactgaccg agaatgcact tgcccacctg gcattgtcca gtctaacgct 750

acctgtgccc ccatacggc gtgtcctgtg ggttgggggtg tgcggaagaa 800

agggacagag actgaggatg tgcggtgtaa gcagtgtgct cggggtacct 850

tctcagatgt gccttctagt gtgatgaaat gcaaagcata cacagactgt 900

ctgagtcaga acctggtggt gatcaagccg gggaccaagg agacagacaa 950

104201-130200







Leu Leu Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln  
 35 40 45  
 Lys Ala Ser Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala  
 50 55 60  
 Thr Gly Gln Val Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr  
 65 70 75  
 Val Ser Glu His Cys Thr Asn Thr Ser Leu Arg Val Cys Ser Ser  
 80 85 90  
 Cys Pro Val Gly Thr Phe Thr Arg His Glu Asn Gly Ile Glu Lys  
 95 100 105  
 Cys His Asp Cys Ser Gln Pro Cys Pro Trp Pro Met Ile Glu Lys  
 110 115 120  
 Leu Pro Cys Ala Ala Leu Thr Asp Arg Glu Cys Thr Cys Pro Pro  
 125 130 135  
 Gly Met Phe Gln Ser Asn Ala Thr Cys Ala Pro His Thr Val Cys  
 140 145 150  
 Pro Val Gly Trp Gly Val Arg Lys Lys Gly Thr Glu Thr Glu Asp  
 155 160 165  
 Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe Ser Asp Val Pro  
 170 175 180  
 Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys Leu Ser Gln  
 185 190 195  
 Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp Asn Val  
 200 205 210  
 Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser Pro  
 215 220 225  
 Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu  
 230 235 240  
 Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu  
 245 250 255  
 Ser Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile  
 260 265 270  
 Gln Glu Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys  
 275 280 285  
 Glu Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His  
 290 295 300  
 Gln Gln Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser  
 305 310 315  
 Met Glu Ala Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly

320	325	330
Pro Lys Arg Gly His	Pro Arg Gln Asn Leu His Lys His Phe Asp	
335	340	345
Ile Asn Glu His Leu	Pro Trp Met Ile Val Leu Phe Leu Leu Leu	
350	355	360
Val Leu Val Val Ile	Val Val Cys Ser Ile Arg Lys Ser Ser Arg	
365	370	375
Thr Leu Lys Lys Gly	Pro Arg Gln Asp Pro Ser Ala Ile Val Glu	
380	385	390
Lys Ala Gly Leu Lys	Lys Ser Met Thr Pro Thr Gln Asn Arg Glu	
395	400	405
Lys Trp Ile Tyr Tyr	Cys Asn Gly His Gly Ile Asp Ile Leu Lys	
410	415	420
Leu Val Ala Ala Gln	Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln	
425	430	435
Phe Leu Cys Asn Ala	Ser Glu Arg Glu Val Ala Ala Phe Ser Asn	
440	445	450
Gly Tyr Thr Ala Asp	His Glu Arg Ala Tyr Ala Ala Leu Gln His	
455	460	465
Trp Thr Ile Arg Gly	Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser	
470	475	480
Ala Leu Arg Gln His	Arg Arg Asn Asp Val Val Glu Lys Ile Arg	
485	490	495
Gly Leu Met Glu Asp	Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala	
500	505	510
Leu Pro Met Ser Pro	Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser	
515	520	525
Pro Asn Ala Lys Leu	Glu Asn Ser Ala Leu Leu Thr Val Glu Pro	
530	535	540
Ser Pro Gln Asp Lys	Asn Lys Gly Phe Phe Val Asp Glu Ser Glu	
545	550	555
Pro Leu Leu Arg Cys	Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu	
560	565	570
Ser Arg Asn Gly Ser	Phe Ile Thr Lys Glu Lys Lys Asp Thr Val	
575	580	585
Leu Arg Gln Val Arg	Leu Asp Pro Cys Asp Leu Gln Pro Ile Phe	
590	595	600
Asp Asp Met Leu His	Phe Leu Asn Pro Glu Glu Leu Arg Val Ile	
605	610	615

Glu Glu Ile Pro Gln Ala Glu Asp Lys Leu Asp Arg Leu Phe Glu  
620 625 630

Ile Ile Gly Val Lys Ser Gln Glu Ala Ser Gln Thr Leu Leu Asp  
635 640 645

Ser Val Tyr Ser His Leu Pro Asp Leu Leu  
650 655

<210> 65

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 65

gtagcagtc acatggggtg ttgg 24

<210> 66

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

accgcacatc ctcatgtctt gtcc 24

<210> 67

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 67

acgatgatcg cgggctccct tctcctgctt ggattcetta gcaccaccac 50

<210> 68

<211> 2412

<212> DNA

<213> Homo sapiens

<400> 68

atgggaagcc agtaacactg tggcctacta tctcttccgt ggtgccatct 50

acatttttgg gactcgggaa ttatgaggta gaggtggagg cggagccgga 100

tgtagaggt cctgaaatag tcacatggg ggaaatgat cgcctgctg 150

ttgaagcccc cttctcattc cgatcgcttt ttggccttga tgattgaaa 200

ataagtctg ttgcaccaga tgcagatgct gttgctgcac agatcctgtc 250

actgctgcca	ttgaagtttt	ttccaatcat	cgtcattggg	atcattgcat	300
tgatattagc	actggccatt	ggtctgggca	tccacttcga	ctgctcaggg	350
aagtacagat	gtcgctcatc	ctttaagtgt	atcgagctga	tagctcgatg	400
tgacggagtc	tcggattgca	aagacgggga	ggacgagtac	cgctgtgtcc	450
gggtgggttg	tcagaatgcc	gtgctccagg	tgttcacagc	tgcttcgttg	500
aagaccatgt	gctccgatga	ctggaagggt	cactacgcaa	atgttgcttg	550
tgcccaactg	ggtttcccaa	gctatgtgag	ttcagataac	ctcagagtga	600
gctcgctgga	ggggcagttc	cgggaggagt	ttgtgtccat	cgatcacctc	650
ttgccagatg	acaaggtgac	tgattacac	cactcagtat	atgtgaggga	700
gggatgtgcc	tctggccacg	tgtttacctt	gcagtgcaca	gcctgtggtc	750
atagaagggg	ctacagctca	cgcatcgtgg	gtggaacat	gtccttgctc	800
tcgcagtggc	cctggcaggc	cagccttcag	ttccagggct	accacctgtg	850
cgggggctct	gtcatcacgc	cctgtgggat	catcactgct	gcacactgtg	900
tttatgactt	gtacctcccc	aagtcatgga	ccatccagggt	gggtctagtt	950
tccctgttgg	acaatccagc	cccatcccac	ttggtggaga	agattgtcta	1000
ccacagcaag	tacaagccaa	agaggctggg	caatgacatc	gcccttatga	1050
agctggccgg	gccactcacg	ttcaatgaaa	tgatccagcc	tgtgtgcctg	1100
cccaactctg	aagagaactt	ccccgatgga	aaagtgtgct	ggacgtcagg	1150
atggggggcc	acagaggatg	gaggtgacgc	ctccccgtgc	ctgaaccacg	1200
cggccgtccc	tttgatttcc	aacaagatct	gcaaccacag	ggacgtgtac	1250
ggtggcatca	tctccccctc	catgctctgc	gcgggctacc	tgacgggttg	1300
cgtggacagc	tgccaggggg	acagcggggg	gcccctggtg	tgtcaagaga	1350
ggaggctgtg	gaagttagtg	ggagcgacca	gctttggcat	cggtgcgca	1400
gaggtgaaca	agcctgggggt	gtacaccctg	gtcacctcct	tcctggactg	1450
gatccacgag	cagatggaga	gagacctaaa	aacctgaaga	ggaagggggac	1500
aagtagccac	ctgagttcct	gaggtgatga	agacagcccg	atcctcccct	1550
ggactcccgt	gtaggaacct	gcacacgagc	agacaccctt	ggagctctga	1600
gttcggcac	cagtagcagg	cccgaagag	gcacccttcc	atctgattcc	1650
agcacaacct	tcaagctgct	ttttgttttt	tgtttttttg	aggtggagtc	1700

tcgctctggt gcccaggctg gaggcagtg gcgaaatccc tgctcactgc 1750  
 agcctccgct tccctgggtc aagcgattct cttgcctcag cttccccagt 1800  
 agctgggacc acaggtgccc gccaccacac ccaactaatt tttgtatttt 1850  
 tagtagagac agggtttcac catgttgccc aggctgctct caaaccctg 1900  
 acctcaaatg atgtgcctgc ttcagcctcc cacagtgtg ggattacagg 1950  
 catgggccac cagcctagc ctcacgtcc tttctgatct tcaactaagaa 2000  
 caaaagaagc agcaacttg aagggcgccc tttccactg gtccatctgg 2050  
 ttttctctcc agggctctgc aaaattctg acgagataag cagttatgtg 2100  
 acctcacgtg caaagccacc aacagccact cagaaaagac gcaccagccc 2150  
 agaagtgcag aactgcagtc actgcacgtt ttcactctca gggaccagaa 2200  
 ccaaaccac cctttctact tccaagactt attttcacat gtggggaggt 2250  
 taatctagga atgactcgtt taaggcctat tttcatgatt tctttgtagc 2300  
 atttggtgct tgacgtatta ttgtccttg attccaaata atatgtttcc 2350  
 ttccctcatt gtctggcgtg tctgcgtgga ctggtgacgt gaatcaaat 2400  
 catccactga aa 2412

<210> 69  
 <211> 453  
 <212> PRT  
 <213> Homo sapiens

<400> 69  
 Met Gly Glu Asn Asp Pro Pro Ala Val Glu Ala Pro Phe Ser Phe  
 1 5 10 15  
 Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala  
 20 25 30  
 Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro  
 35 40 45  
 Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile  
 50 55 60  
 Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly  
 65 70 75  
 Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala  
 80 85 90  
 Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr  
 95 100 105  
 Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe

	110	115	120
Thr Ala Ala Ser	Trp Lys Thr Met Cys	Ser Asp Asp Trp Lys Gly	
	125	130	135
His Tyr Ala Asn	Val Ala Cys Ala Gln	Leu Gly Phe Pro Ser Tyr	
	140	145	150
Val Ser Ser Asp	Asn Leu Arg Val Ser	Ser Leu Glu Gly Gln Phe	
	155	160	165
Arg Glu Glu Phe	Val Ser Ile Asp His	Leu Leu Pro Asp Asp Lys	
	170	175	180
Val Thr Ala Leu	His His Ser Val Tyr	Val Arg Glu Gly Cys Ala	
	185	190	195
Ser Gly His Val	Val Thr Leu Gln Cys	Thr Ala Cys Gly His Arg	
	200	205	210
Arg Gly Tyr Ser	Ser Arg Ile Val Gly	Gly Asn Met Ser Leu Leu	
	215	220	225
Ser Gln Trp Pro	Trp Gln Ala Ser Leu	Gln Phe Gln Gly Tyr His	
	230	235	240
Leu Cys Gly Gly	Ser Val Ile Thr Pro	Leu Trp Ile Ile Thr Ala	
	245	250	255
Ala His Cys Val	Tyr Asp Leu Tyr Leu	Pro Lys Ser Trp Thr Ile	
	260	265	270
Gln Val Gly Leu	Val Ser Leu Leu Asp	Asn Pro Ala Pro Ser His	
	275	280	285
Leu Val Glu Lys	Ile Val Tyr His Ser	Lys Tyr Lys Pro Lys Arg	
	290	295	300
Leu Gly Asn Asp	Ile Ala Leu Met Lys	Leu Ala Gly Pro Leu Thr	
	305	310	315
Phe Asn Glu Met	Ile Gln Pro Val Cys	Leu Pro Asn Ser Glu Glu	
	320	325	330
Asn Phe Pro Asp	Gly Lys Val Cys Trp	Thr Ser Gly Trp Gly Ala	
	335	340	345
Thr Glu Asp Gly	Gly Asp Ala Ser Pro	Val Leu Asn His Ala Ala	
	350	355	360
Val Pro Leu Ile	Ser Asn Lys Ile Cys	Asn His Arg Asp Val Tyr	
	365	370	375
Gly Gly Ile Ile	Ser Pro Ser Met Leu	Cys Ala Gly Tyr Leu Thr	
	380	385	390
Gly Gly Val Asp	Ser Cys Gln Gly Asp	Ser Gly Gly Pro Leu Val	
	395	400	405

10047084-10404



Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe  
 410 415 420

Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg  
 425 430 435

Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp  
 440 445 450

Leu Lys Thr

<210> 70  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 70  
 tgacatcgcc cttatgaagc tggc 24

<210> 71  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 71  
 .tacacgtccc tgtggttgca gatc 24

<210> 72  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 72  
 cgttcaatgc agaaatgatc cagcctgtgt gctgcccac ctctgaagag 50

<210> 73  
 <211> 3305  
 <212> DNA  
 <213> Homo sapiens

<400> 73  
 cccacgcgtc cgtcctagtc cccgggcccac ctcgacagtt ttgctcattt 50  
 attgcaacgg tcaaggctgg cttgtgccag aacggcgcgc gcgcgcgcac 100  
 gcacgcacac acacgggggg aaactttttt aaaaatgaaa ggctagaaga 150  
 gctcagcggc ggcgcgggcg ctgcgcgagg gctccggagc tgactcgccg 200

aggcaggaaa tccctccggt cgcgacgcc ggccccgggt cggcgccgc 250  
 gtgggatggt gcagcgctcg ccgccgggcc cgagagctgc tgactgaag 300  
 gccggcgacg atggcagcgc gcccgctgcc cgtgtcccc gcccgcgccc 350  
 tctgtctgc cctggccggt gctctgctcg cgccctgcga ggcccgagg 400  
 gtgagcttat ggaaccaagg aagagctgat gaagttgtca gtgcctctgt 450  
 tcggagtggg gacctctgga tcccagtga gagcttcgac tccaagaatc 500  
 atccagaagt gctgaatatt cgactacaac gggaaagcaa agaactgatc 550  
 ataaatctgg aaagaaatga aggtctcatt gccagcagtt tcacggaaac 600  
 ccactatctg caagacggta ctgatgtctc cctcgctcga aattacacgg 650  
 gtcactgtta ctaccatgga catgtacggg gatattctga ttcagcagtc 700  
 agtctcagca cgtgttctgg tctcagggga cttattgtgt ttgaaatga 750  
 aagctatgtc ttagaaccaa tgaaaagtgc aaccaacaga taaaaactct 800  
 tcccagcgaa gaagctgaaa agcgtccggg gatcatgtgg atcacatcac 850  
 aacacaccaa acctcgctgc aaagaatgtg tttccaccac cctctcagac 900  
 atgggcaaga aggcataaaa gagagaccct caaggcaact aagtatgtgg 950  
 agctggtgat cgtggcagac aaccgagagt ttcagaggca aggaaaagat 1000  
 ctggaaaaag ttaagcagcg attaatagag attgctaata acgttgacaa 1050  
 gttttacaga ccactgaaca ttcggatcgt gttggtaggc gtggaagtgt 1100  
 ggaatgacat ggacaaatgc tctgtaagtc aggaccatt caccagcctc 1150  
 catgaatttc tggactggag gaagatgaag cttctacctc gcaaatccca 1200  
 tgacaatgcg cagcttgtca gtggggttta tttccaagg accaccatcg 1250  
 gcatggcccc aatcatgagc atgtgcacgg cagaccagtc tgggggaatt 1300  
 gtcattggacc attcagacaa tccccttggg gcagccgtga ccctggcaca 1350  
 tgagctgggc cacaatttcg ggatgaatca tgacacactg gacaggggct 1400  
 gtagctgtca aatggcgggt gagaaaggag gctgcatcat gaacgcttcc 1450  
 accgggtacc catttcccat ggtgttcagc agttgcagca ggaaggactt 1500  
 ggagaccagc ctggagaaaag gaatgggggt gtgcctgttt aacctgccg 1550  
 aagtcaggga gtctttcggg ggccagaagt gtgggaacag atttgtggaa 1600  
 gaaggagagg agtgtgactg tggggagcca gaggaatgta tgaatcgctg 1650



gagaaagggc ggtgaactct ggctctttgc tgtggacatg cgtgaccagc 3150  
 agtactcagg tttgagggtt .tgcagaaagc cagggaaccc acagagtcac 3200  
 caaccttca ttttaacaagt aagaatgtta aaaagtgaaa acaatgtaag 3250  
 agcctaactc catcccccggt ggccattact gcataaaata gaggcattt 3300  
 gaaat 3305

<210> 74  
 <211> 735  
 <212> PRT  
 <213> Homo sapiens

<400> 74

Met	Ala	Ala	Arg	Pro	Leu	Pro	Val	Ser	Pro	Ala	Arg	Ala	Leu	Leu	1	5	10	15
Leu	Ala	Leu	Ala	Gly	Ala	Leu	Leu	Ala	Pro	Cys	Glu	Ala	Arg	Gly	20	25	30	
Val	Ser	Leu	Trp	Asn	Gln	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala	35	40	45	
Ser	Val	Arg	Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp	50	55	60	
Ser	Lys	Asn	His	Pro	Glu	Val	Leu	Asn	Ile	Arg	Leu	Gln	Arg	Glu	65	70	75	
Ser	Lys	Glu	Leu	Ile	Ile	Asn	Leu	Glu	Arg	Asn	Glu	Gly	Leu	Ile	80	85	90	
Ala	Ser	Ser	Phe	Thr	Glu	Thr	His	Tyr	Leu	Gln	Asp	Gly	Thr	Asp	95	100	105	
Val	Ser	Leu	Ala	Arg	Asn	Tyr	Thr	Gly	His	Cys	Tyr	Tyr	His	Gly	110	115	120	
His	Val	Arg	Gly	Tyr	Ser	Asp	Ser	Ala	Val	Ser	Leu	Ser	Thr	Cys	125	130	135	
Ser	Gly	Leu	Arg	Gly	Leu	Ile	Val	Phe	Glu	Asn	Glu	Ser	Tyr	Val	140	145	150	
Leu	Glu	Pro	Met	Lys	Ser	Ala	Thr	Asn	Arg	Tyr	Lys	Leu	Phe	Pro	155	160	165	
Ala	Lys	Lys	Leu	Lys	Ser	Val	Arg	Gly	Ser	Cys	Gly	Ser	His	His	170	175	180	
Asn	Thr	Pro	Asn	Leu	Ala	Ala	Lys	Asn	Val	Phe	Pro	Pro	Pro	Ser	185	190	195	
Gln	Thr	Trp	Ala	Arg	Arg	His	Lys	Arg	Glu	Thr	Leu	Lys	Ala	Thr	200	205	210	

protein = 45021001

Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln  
215 220 225

Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu  
230 235 240

Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg  
245 250 255

Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys  
260 265 270

Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp  
275 280 285

Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala  
290 295 300

Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met  
305 310 315

Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile  
320 325 330

Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu  
335 340 345

Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu  
350 355 360

Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys  
365 370 375

Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser  
380 385 390

Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met  
395 400 405

Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly  
410 415 420

Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys  
425 430 435

Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala  
440 445 450

Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu  
455 460 465

Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg  
470 475 480

Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala  
485 490 495

Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser



tcccaaggct tcttgatgg cagatgattn tggggttttg cattgtttcc 50  
 ctgacaacga aaacaaaaca gttttggggg ttcaggaggg gaantccagc 100  
 ctaccagga agtttgcaga aacagtgcaa ggaagggcag ganttcctgg 150  
 ttgagntttt tgntaaaaca tggacatgnt tcagtgtgc tcntgagaga 200  
 gtagcagggt accacttttg gcaggcccca gccctgcagc aaggaggaag 250  
 aggactcaaa agtttggcct ttcactgagc ctccacagca gtgggggaga 300  
 agcaagggtt gggcccagtg tcccctttcc ccagtgcac ctcagccttg 350  
 gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400  
 tttagcattt attatatgaa aatagcaggg ttttagtttt taatttatca 450  
 gagaccctgc caccattcc atntccatcc aag 483

<210> 76  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 76  
 gtctcagcac gtgttctggt ctcaggg 27

<210> 77  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 77  
 catgagcatg tgcacggc 18

<210> 78  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 78  
 tacctgcacg atgggcac 18

<210> 79  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

Sequence: 18027001

<220>  
<223> Synthetic oligonucleotide probe

<400> 79  
cactgggcac ctcccttc 18

<210> 80  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 80  
ctccaggctg gtctccaagt ccttcc 26

<210> 81  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 81  
tccctgttg actctgcagc ttcc 24

<210> 82  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 82  
cttcgctggg aagagtttg 19

<210> 83  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 83  
gtgcaaccaa cagatacaaa ctcttccag cgaagaagct gaaaagcgtc 50

<210> 84  
<211> 1714  
<212> DNA  
<213> Homo sapiens

<400> 84  
catcctgcaa catggtgaaa ccacgcctgg ctaattttgt tgtatttttg 50



gtagagatgg gatttcaccg tgtagccag gattgtctca atctgacctc 100  
atgatctgcc cgcctcggcc tcccaaagtg ctgggattac aggcgagtgc 150  
aaccacaccc ggccacaaac tttttaagaa gttaatgaaa ccataccttt 200  
tacattttta atgacaggaa aatgctcaca ataattgtta acccaaaatt 250  
ctggatacaa aagtacaatc ttactgtgt aaatacatgt atatgtacta 300  
tatgaaaata taccaaatat caataatact tatctctggg taaaaacctc 350  
ttctcatacc ctgtgctaac aacttttaac aaaaaatttg catcactttt 400  
aagaatcaag aaaaatttct gaaggtcata tgggacagaa aaaaaacca 450  
agggaaaaat cagccactt gggaaaaaaa gattcgaaat ctgccttttt 500  
atagatttgt aattaataag gtccaggctt tctaagcaac ttaaattgtt 550  
tgtttcgaaa caaagtactt gtctggatgt aggaggaaag ggagtgatgt 600  
cactgccatt atgatgcccc ttgaatataa gacctactt gctatctccc 650  
ctgcaccagc caggagccac ccactctcca gcacactgag cagcaagctg 700  
gacacacggc aactgatcc aaatgggtaa ggggatggtg gcgatgctca 750  
ttctgggtct gctacttctg gcgctgctcc taccctgca ggtttcttca 800  
tttgttcctt taaccagtat gccggaagct actgcagccg aaaccacaaa 850  
gcctccaac agtgcctac agcctacagc cggctctctt gtggtcttgc 900  
ttgcccttct acatctctac cattaagagg caggtaaga aacagctaca 950  
gttctccaac ccatacacta aaaccgaatc caaatgggta ctagaagttc 1000  
aatgtggcaa ggaaaaaac caggtcttca tcaaactctac taatttcaact 1050  
ccttattaac agagaaacgc ttgagagtct caaactggac tggtttaaag 1100  
agcatctgaa ggatttgact agatgataaa tgctgtact ccagtaactt 1150  
tgaggagcct aggcggcgg atcacctgag gtcaggagt ttgagactaac 1200  
ctggccaaaa tggtgaaacc ccactgtac taaaaatata aatattgact 1250  
ggcggtggtg gtgagtgcct gtgatcccag ctactcaggt ggctgaagca 1300  
ggacaatcac ttgaactcag gaggcagagg ttgcagtga ctgagatgc 1350  
gctactgcac tctagcctag cctgggcaac agagtgaac ttcgtctcaa 1400  
aaaaaaaaa gccaaagtga gtggtcacg cctgtaatcc cggcactttg 1450  
ggaggccgag gtggcggtat cagaggtca ggagatcaag accatcctgg 1500

ctaatacagt gaaaccctgt ctctactaaa aatacaaaaa attagccggg 1550  
gatggtggca ggcacctgga gtcccagcta ctcgggaggc tgaggcagga 1600  
gaatagcgtg aactcaggag gggagccttg cagttagccg agattgcgct 1650  
actgcactcc agcctgggag acagcgcgag actccgtctc aaaaaaaaaa 1700  
aaaaaaaaaa aaaa 1714

<210> 85  
<211> 67  
<212> PRT  
<213> Homo sapiens

<400> 85  
Met Gly Lys Gly Met Val Ala Met Leu Ile Leu Gly Leu Leu Leu  
1 5 10 15  
Leu Ala Leu Leu Leu Pro Val Gln Val Ser Ser Phe Val Pro Leu  
20 25 30  
Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser  
35 40 45  
Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu  
50 55 60  
Ala Leu Leu His Leu Tyr His  
65

Feature = table

<210> 86  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 86  
acgggcacac tggatcccaa atg 23

<210> 87  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 87  
ggtagagatg tagaaggcca agcaagacc 29

<210> 88  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 88  
gctccctacc cgtgcaggtt ttttcatttg ttcctttaac cagtatgccg 50

<210> 89  
<211> 2956  
<212> DNA  
<213> Homo sapiens

<400> 89  
gccgcggcga gagcgcgccc agccccgccg cgatgcccgc gcgcccagga 50  
cgcctcctcc cgctgctggc ccggccggcg gccctgactg cgctgctgct 100  
gctgctgctg ggccatggcg gcggcgggcg ctggggcgcc cggggcccagg 150  
aggcggcggc ggcgcgggcg gacggggccc ccgcggcaga cggcgaggac 200  
ggacaggacc cgcacagcaa gcacctgtac acggccgaca tgttcacgca 250  
cgggatccag agcgcgcgcg acttcgtcat gttcttcgcg ccctggtgtg 300  
gacactgcc a gcggtgcag ccgacttga atgacctggg agacaaatac 350  
aacagcatgg aagatgccaa agtctatgtg gctaaagtgg actgcacggc 400  
ccactccgac gtgtgctccg cccagggggg gcgaggatac cccaccttaa 450  
agcttttcaa gccaggccaa gaagctgtga agtaccaggg tcctcgggac 500  
ttccagacac tggaaaactg gatgctgcag aactgaacg aggagccagt 550  
gacaccagag ccggaagtgg aaccgcccag tgcccccgag ctcaagcaag 600  
ggctgtatga gctctcagca agcaactttg agctgcacgt tgcacaaggc 650  
gaccacttta tcaagttctt cgctccgtgg tgtggtcact gcaaagccct 700  
ggctccaacc tgggagcagc tggctctggg ccttgaacat tccgaaactg 750  
tcaagattgg caaggttgat tgtacacagc actatgaact ctgctccgga 800  
aaccagggtt gtggtatcc cactcttctc tgggtccgag atgggaaaaa 850  
ggtggatcag tacaaggga agcgggattt ggagtcactg agggagtacg 900  
tggagtcgca gctgcagcgc acagagactg gagcgacgga gaccgtcacg 950  
ccctcagagg ccccggtgct ggcagctgag cccgaggtg acaagggcac 1000  
tgtgttggca ctactgaaa ataacttca tgacaccatt gcagaaggaa 1050  
taaccttcat caagttttat gctccatggt gtggtcattg taagactctg 1100  
gctcctactt gggaggaact ctctaaaaag gaattccctg gtctggcggg 1150



tgcaccaac actcttcacc cacctcccat acgcaagggg atgtggatac 2650  
 ttggcccaaa gtaactggtg gtaggaatct tagaacaag accacttata 2700  
 ctgtctgtct gaggcagaag ataacagcag catctcgacc agcctctgcc 2750  
 ttaaaggaaa tctttattaa tcacgtatgg ttcacagata attctttttt 2800  
 taaaaaaacc caacctccta gagaagcaca actgtcaaga gtcttgtaca 2850  
 cacaacttca gctttgcac acgagtcttg tattccaaga aaatcaaagt 2900  
 ggtacaattt gtttgtttac actatgatac tttctaaata aactcttttt 2950  
 ttttaa 2956

<210> 90  
 <211> 432  
 <212> PRT  
 <213> Homo sapiens

<400> 90  
 Met Pro Ala Arg Pro Gly Arg Leu Leu Pro Leu Leu Ala Arg Pro  
 1 5 10 15  
 Ala Ala Leu Thr Ala Leu Leu Leu Leu Leu Gly His Gly Gly  
 20 25 30  
 Gly Gly Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala Ala  
 35 40 45  
 Ala Asp Gly Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro  
 50 55 60  
 His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile  
 65 70 75  
 Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly  
 80 85 90  
 His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys  
 95 100 105  
 Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp  
 110 115 120  
 Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly  
 125 130 135  
 Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys  
 140 145 150  
 Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu  
 155 160 165  
 Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu  
 170 175 180

Protein = 4302400

Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	Glu	Leu	Ser	185	190	195
Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile	200	205	210
Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro	215	220	225
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val	230	235	240
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser	245	250	255
Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp	260	265	270
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser	275	280	285
Leu	Arg	Glu	Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly	290	295	300
Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala	305	310	315
Glu	Pro	Glu	Ala	Asp	Lys	Gly	Thr	Val	Leu	Ala	Leu	Thr	Glu	Asn	320	325	330
Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe	335	340	345
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp	350	355	360
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys	365	370	375
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys	380	385	390
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly	395	400	405
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu	410	415	420
His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu				425	430	

- <210> 91
- <211> 20
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe

<400> 91  
atgttcttcg cgccctggtg 20

<210> 92  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 92  
ccaagccaac acactctaca g 21

<210> 93  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 93  
aagtggtcgc cttgtgcaac gtgc 24

<210> 94  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 94  
ggtcaaagg gatatatcgc cac 23

<210> 95  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 95  
gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggcca 49

<210> 96  
<211> 1016  
<212> DNA  
<213> Homo sapiens

<400> 96  
cttttctgag gaaccacagc aatgaatggc tttgcatcct tgcttogaag 50  
aaaccaattt atcctcctgg tactatttct tttgcaaatt cagagtctgg 100  
gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150





80	85	90
Thr Gly Pro Ile Gly Lys Lys Gly Asp	Lys Gly Glu Lys Gly Leu	
95	100	105
Leu Gly Ile Pro Gly Glu Lys Gly Lys	Ala Gly Thr Val Cys Asp	
110	115	120
Cys Gly Arg Tyr Arg Lys Phe Val Gly	Gln Leu Asp Ile Ser Ile	
125	130	135
Ala Arg Leu Lys Thr Ser Met Lys Phe	Val Lys Asn Val Ile Ala	
140	145	150
Gly Ile Arg Glu Thr Glu Glu Lys Phe	Tyr Tyr Ile Val Gln Glu	
155	160	165
Glu Lys Asn Tyr Arg Glu Ser Leu Thr	His Cys Arg Ile Arg Gly	
170	175	180
Gly Met Leu Ala Met Pro Lys Asp Glu	Ala Ala Asn Thr Leu Ile	
185	190	195
Ala Asp Tyr Val Ala Lys Ser Gly Phe	Phe Arg Val Phe Ile Gly	
200	205	210
Val Asn Asp Leu Glu Arg Glu Gly Gln	Tyr Met Ser Thr Asp Asn	
215	220	225
Thr Pro Leu Gln Asn Tyr Ser Asn Trp	Asn Glu Gly Glu Pro Ser	
230	235	240
Asp Pro Tyr Gly His Glu Asp Cys Val	Glu Met Leu Ser Ser Gly	
245	250	255
Arg Trp Asn Asp Thr Glu Cys His Leu	Thr Met Tyr Phe Val Cys	
260	265	270
Glu Phe Ile Lys Lys Lys Lys		
275		

<210> 98  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 98  
 cgctgactat gttgccaaga gtgg 24  
  
 <210> 99  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>

<223> Synthetic oligonucleotide probe

<400> 99

gatgatggag gctccatacc tcag 24

<210> 100

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 100

gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 101

ggttctatcg attcgaattc ggccacactg gccggatcct ctagagatcc 50

ctcgacctcg acccacgcgt ccgctgctct ccgcccgtgt ggagtgggtg 100

gggcctgggt gggaatgggc gtgtgccagc gcacgcgcgc tccctggaag 150

gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200

agggatgttt gcgagcggct ggaaccagac ggtgccgata gaggaagcgg 250

gctccatggc tgcctcctg ctgtgcccc tgctgctgtt gctaccgctg 300

ctgtgctga agctacacct ctggccgag ttgcgctggc ttccggcgga 350

cttgcccttt gcggtgcgag ctctgtgctg caaaagggt cttcgagctc 400

gcgccctggc cgcggtgcc gccgaccgg aaggtcccga ggggggctgc 450

agcctggcct gggcctcgc ggaactggc cagcagcgc ccgcgcacac 500

ctttctcatt cacggctcgc ggcgcttttag ctactcagag gcggagcgcg 550

agagtaacag ggctgcacgc gccttcctac gtgcgctagg ctgggactgg 600

ggacccgacg gcggcgacag cggcgagggg agcgtggag aaggcgagcg 650

ggcagcgccg ggagccggag atgcagcggc cggaagcggc gcggagtgtg 700

ccggagggga cggtgccgcc agaggtggag gagccgccgc ccctctgtca 750

cctggagcaa ctgtggcgct gctcctcccc gctggcccag agtttctgtg 800

gctctgttgc gggtggcca aggccggcct gcgcactgcc tttgtgccca 850

ccgccctgcg ccggggcccc ctgtgcact gcctccgag ctgcggcgcg 900

cgcgcgctgg tgctggcgcc agagtttctg ggtccctgg agccggacct 950  
 gcccgccttg agagccatgg ggctccacct gtgggctgca ggcccaggaa 1000  
 cccaccctgc tggaattagc gatttgctgg ctgaagtgtc cgctgaagtg 1050  
 gatgggccag tgccaggata cctctcttcc cccagagca taacagacac 1100  
 gtgctgtac atcttcacct ctggcaccac gggcctccc aaggtgctc 1150  
 ggatcagtca tctgaagatc ctgcaatgcc agggcttcta tcagctgtgt 1200  
 ggtgtccacc aggaagatgt gatctacctc gccctccac tctaccacat 1250  
 gtccggttcc ctgctgggca tctggtgctg catgggcatt ggggccacag 1300  
 tgggtctgaa atccaagttc tgggtggtc agttctggga agattgccag 1350  
 cagcacaggg tgacggtgtt ccagtacatt ggggagctgt gccgatacct 1400  
 tgtcaaccag ccccgagca aggcagaacg tggccataag gtccggctgg 1450  
 cagtgggcag cgggctgcgc ccagatacct gggagcgttt tgtgcggcgc 1500  
 ttcgggcccc tgcaggtgct ggagacatat ggactgacag agggcaacgt 1550  
 ggccaccatc aactacacag gacagcgggg cgctgtgggg cgtgcttctc 1600  
 ggctttacaa gcatacttcc ccttctctct tgattcgcta tgatgtcacc 1650  
 acaggagagc caattcggga ccccgagggg cactgtatgg ccacatctcc 1700  
 aggtgagcca gggctgctgg tggccccggt aagccagcag tccccattcc 1750  
 tgggctatgc tggcgggcca gagctggccc aggggaagtt gctaaaggat 1800  
 gtcttccggc ctggggatgt tttcttcaac actggggacc tctgtgtctg 1850  
 cgatgaccaa ggttttctcc gcttccatga tcgtactgga gacaccttca 1900  
 ggtggaaggg ggagaatgtg gccacaaccg aggtggcaga ggtcttcgag 1950  
 gccctagatt ttcttcagga ggtgaacgtc tatggagtca ctgtgccagg 2000  
 gcatgaaggc agggctggaa tggcagccct agttctgcgt cccccccagc 2050  
 ctttggaacct tatgcagctc tacaccacag tgtctgagaa cttgccacct 2100  
 tatgcccggc cccgattcct caggtccag gagtcttgg ccaccacaga 2150  
 gaccttcaaa cagcagaaag ttcggatggc aaatgagggc ttcgacccca 2200  
 gcaccctgtc tgaccactg tacgttctgg accaggctgt aggtgcctac 2250  
 ctgccccctc caactgccg gtacagcgc ctctggcag gaaaccttcg 2300  
 aatctgagaa cttccacacc tgaggcacct gagagaggaa ctctgtgggg 2350

tgggggccgt tgcagggtga ctgggctgtc agggatcttt tctataccag 2400  
 aactgcggtc actatcttgt aataaatgtg gctggagctg atccagctgt 2450  
 ctctgacctt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa ggcggccgcg 2500  
 actctagagt cgacctgcag tagggataac agggtaataa gcttggccgc 2550  
 catggcccaa ctgttttatt gcag 2574

<210> 102  
 <211> 730  
 <212> PRT  
 <213> Homo sapiens

<400> 102

Met	Gly	Val	Cys	Gln	Arg	Thr	Arg	Ala	Pro	Trp	Lys	Glu	Lys	Ser
1				5					10					15
Gln	Leu	Glu	Arg	Ala	Ala	Leu	Gly	Phe	Arg	Lys	Gly	Gly	Ser	Gly
				20					25					30
Met	Phe	Ala	Ser	Gly	Trp	Asn	Gln	Thr	Val	Pro	Ile	Glu	Glu	Ala
				35					40					45
Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu
				50					55					60
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp
				65					70					75
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys
				80					85					90
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Asp	Pro	
				95					100					105
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu
				110					115					120
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser
				125					130					135
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala
				140					145					150
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp
				155					160					165
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala
				170					175					180
Ala	Pro	Gly	Ala	Gly	Asp	Ala	Ala	Ala	Gly	Ser	Gly	Ala	Glu	Phe
				185					190					195
Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro
				200					205					210

Leu Ser Pro Gly	Ala Thr Val Ala Leu	Leu Leu Pro Ala Gly	Pro
215		220	225
Glu Phe Leu Trp	Leu Trp Phe Gly Leu	Ala Lys Ala Gly Leu	Arg
230		235	240
Thr Ala Phe Val	Pro Thr Ala Leu Arg	Arg Gly Pro Leu Leu	His
245		250	255
Cys Leu Arg Ser	Cys Gly Ala Arg Ala	Leu Val Leu Ala Pro	Glu
260		265	270
Phe Leu Glu Ser	Leu Glu Pro Asp Leu	Pro Ala Leu Arg Ala	Met
275		280	285
Gly Leu His Leu	Trp Ala Ala Gly Pro	Gly Thr His Pro Ala	Gly
290		295	300
Ile Ser Asp Leu	Leu Ala Glu Val Ser	Ala Glu Val Asp Gly	Pro
305		310	315
Val Pro Gly Tyr	Leu Ser Ser Pro Gln	Ser Ile Thr Asp Thr	Cys
320		325	330
Leu Tyr Ile Phe	Thr Ser Gly Thr Thr	Gly Leu Pro Lys Ala	Ala
335		340	345
Arg Ile Ser His	Leu Lys Ile Leu Gln	Cys Gln Gly Phe Tyr	Gln
350		355	360
Leu Cys Gly Val	His Gln Glu Asp Val	Ile Tyr Leu Ala Leu	Pro
365		370	375
Leu Tyr His Met	Ser Gly Ser Leu Leu	Gly Ile Val Gly Cys	Met
380		385	390
Gly Ile Gly Ala	Thr Val Val Leu Lys	Ser Lys Phe Ser Ala	Gly
395		400	405
Gln Phe Trp Glu	Asp Cys Gln Gln His	Arg Val Thr Val Phe	Gln
410		415	420
Tyr Ile Gly Glu	Leu Cys Arg Tyr Leu	Val Asn Gln Pro Pro	Ser
425		430	435
Lys Ala Glu Arg	Gly His Lys Val Arg	Leu Ala Val Gly Ser	Gly
440		445	450
Leu Arg Pro Asp	Thr Trp Glu Arg Phe	Val Arg Arg Phe Gly	Pro
455		460	465
Leu Gln Val Leu	Glu Thr Tyr Gly Leu	Thr Glu Gly Asn Val	Ala
470		475	480
Thr Ile Asn Tyr	Thr Gly Gln Arg Gly	Ala Val Gly Arg Ala	Ser
485		490	495
Trp Leu Tyr Lys	His Ile Phe Pro Phe	Ser Leu Ile Arg Tyr	Asp

Protein Data Bank

500	505	510
Val Thr Thr Gly Glu Pro Ile Arg Asp	Pro Gln Gly His Cys Met	
515	520	525
Ala Thr Ser Pro Gly Glu Pro Gly Leu	Leu Val Ala Pro Val Ser	
530	535	540
Gln Gln Ser Pro Phe Leu Gly Tyr Ala	Gly Gly Pro Glu Leu Ala	
545	550	555
Gln Gly Lys Leu Leu Lys Asp Val Phe	Arg Pro Gly Asp Val Phe	
560	565	570
Phe Asn Thr Gly Asp Leu Leu Val Cys	Asp Asp Gln Gly Phe Leu	
575	580	585
Arg Phe His Asp Arg Thr Gly Asp Thr	Phe Arg Trp Lys Gly Glu	
590	595	600
Asn Val Ala Thr Thr Glu Val Ala Glu	Val Phe Glu Ala Leu Asp	
605	610	615
Phe Leu Gln Glu Val Asn Val Tyr Gly	Val Thr Val Pro Gly His	
620	625	630
Glu Gly Arg Ala Gly Met Ala Ala Leu	Val Leu Arg Pro Pro His	
635	640	645
Ala Leu Asp Leu Met Gln Leu Tyr Thr	His Val Ser Glu Asn Leu	
650	655	660
Pro Pro Tyr Ala Arg Pro Arg Phe Leu	Arg Leu Gln Glu Ser Leu	
665	670	675
Ala Thr Thr Glu Thr Phe Lys Gln Gln	Lys Val Arg Met Ala Asn	
680	685	690
Glu Gly Phe Asp Pro Ser Thr Leu Ser	Asp Pro Leu Tyr Val Leu	
695	700	705
Asp Gln Ala Val Gly Ala Tyr Leu Pro	Leu Thr Thr Ala Arg Tyr	
710	715	720
Ser Ala Leu Leu Ala Gly Asn Leu Arg	Ile	
725	730	

<210> 103

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

gagagccatg gggctccacc tg 22

<210> 104  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 104  
ggagaatgtg gccacaac 18

<210> 105  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 105  
gccctggcac agtgactcca tagacg 26

<210> 106  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 106  
atccacttca gcggacac 18

<210> 107  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 107  
ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108  
<211> 2579  
<212> DNA  
<213> Homo sapiens

<400> 108  
cctgtgttaa gctgaggttt cccctagatc tcgtatatcc ccaacacata 50  
cctccacgca cacacatccc caagaacctc gagtcacac caacagacac 100  
acgcgcgcat acacactcgc tctcgcttgt ccatctccct cccgggggag 150  
ccggcgcgag ctccacactt tgccgcacac tccggcgagc cgagcccgca 200

gcgctccagg attctgcggc tcggaactcg gattgcagct ctgaaccccc 250  
atggtgggtt tttaaact tcttttctt ctcttctcg ttttgattgc 300  
accgtttcca tctgggggct agaggagcaa ggcagcagcc ttcccagcca 350  
gcccttggtg gcttgccatc gtccatctgg cttataaaag tttgctgagc 400  
gcagtccaga gggctgcgct gctcgtcccc tcggttgga gaagggggtg 450  
acgctgggca gggcgagga gcgcgcgct gcctctggcg ggctttcggc 500  
ttgaggggca aggtgaagag cgcaccggcc gtgggggtta ccgagctgga 550  
tttgatgtt gcaccatgcc ttcttgatc ggggtgtga ttcttccct 600  
cttggggctg ctgctctccc tccccgcgg ggcgatgtg aaggctcga 650  
gctgcggaga ggtccgccag gcgtacggtg ccaagggatt cagcctggcg 700  
gacatcccct accaggagat cgcaggggaa cacttaagaa tctgtcctca 750  
ggaatataca tgctgcacca cagaaatgga agacaagtta agccaacaaa 800  
gcaaactcga atttgaaaac cttgtggaag agacaagcca tttgtgcgc 850  
accacttttg tgtccaggca taagaaattt gacgaatttt tccgagagct 900  
cctggagaat gcagaaaagt cactaaatga tatgtttgta cggacctatg 950  
gcatgctgta catgcagaat tcagaagtct tccaggacct cttcacagag 1000  
ctgaaaaggt actacactgg gggtaatgtg aatctggagg aaatgctcaa 1050  
tgacttttgg gctcggctcc tggaaaggat gtttcagctg ataaaccctc 1100  
agtatcactt cagtgaagac tacctggaat gtgtgagcaa atacactgac 1150  
cagctcaagc catttggaag cgtgccccgg aaactgaaga ttcaggttac 1200  
ccgcgccttc attgctgcca ggacctttgt ccaggggctg actgtgggca 1250  
gagaagttgc aaaccgagtt tccaagggtc gcccaacccc aggggtgtatc 1300  
cgtgccctca tgaagatgct gtactgccca tactgtcggg ggcttccac 1350  
tgtgaggccc tgcaacaact actgtctcaa cgtcatgaag ggctgcttg 1400  
caaatcaggc tgacctgac acagagtga atctgtttat agatgcaatg 1450  
ctcttggtgg cagagcgact ggaggggcca ttcaacattg agtcggtcat 1500  
ggacccgata gatgtcaaga tttctgaagc cattatgaac atgcaagaaa 1550  
acagcatgca ggtgtctgca aaggtcttcc agggatgtgg tcagcccaaa 1600  
cctgctccag ccctcagatc tgcccgtca gctcctgaaa attttaatac 1650



acgttttcagg ccctacaatc ctgaggaaag accaacaact gctgcaggca 1700  
 caagcttggg cgggctgggc acagacataa aagagaaatt gaagctctct 1750  
 aaaaagggtct ggtcagcatt accctacact atctgcaagg acgagagcgt 1800  
 gacagcgggc acgtccaacg aggaggaatg ctggaacggg cacagcaaag 1850  
 ccagatactt gcctgagatc atgaatgatg ggctcaccaa ccagatcaac 1900  
 aatcccgagg tggatgtgga catcactcgg cctgacactt tcacagaca 1950  
 gcagattatg gctctccgtg tgatgaccaa caaactaaaa aacgcctaca 2000  
 atggcaatga tgtcaatttc caggacacaa gtgatgaatc cagtggctca 2050  
 gggagtggca gtgggtgcat ggatgacgtg tgtcccacgg agtttgagtt 2100  
 tgtcaccaca gaggcccccg cagtggatcc cgaccggaga gaggtggact 2150  
 cttctgcagc ccagcgtggc cactccctgc tctcctgggc tctcacctgc 2200  
 attgtcctgg cactgcagag actgtgcaga taatcttggg tttttgtca 2250  
 gatgaaactg cattttagct atctgaatgg ccaactcact tcttttctta 2300  
 cactcttggg caatggacca tgccacaaaa acttaccgtt ttctatgaga 2350  
 agagagcagt aatgcaatct gcctcccttt ttgttttccc aaagagtacc 2400  
 gggtgccaga ctgaactgct tcctctttcc ttcagctatc tgtggggacc 2450  
 ttgtttattc tagagagaat tcttactcaa atttttcgta ccaggagatt 2500  
 ttottacctt catttgcttt tatgctgcag aagtaaagga atctcacgtt 2550  
 gtgagggttt ttttttctc atttaaaat 2579

<210> 109  
 <211> 555  
 <212> PRT  
 <213> Homo sapiens

<400> 109  
 Met Pro Ser Trp Ile Gly Ala Val Ile Leu Pro Leu Leu Gly Leu  
 1 5 10 15  
 Leu Leu Ser Leu Pro Ala Gly Ala Asp Val Lys Ala Arg Ser Cys  
 20 25 30  
 Gly Glu Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala  
 35 40 45  
 Asp Ile Pro Tyr Gln Glu Ile Ala Gly Glu His Leu Arg Ile Cys  
 50 55 60  
 Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu  
 65 70 75

Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	80	85	90
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	95	100	105
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	125	130	135
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150
Thr	Gly	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	Leu	Asn	Asp	Phe	Trp	155	160	165
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Gln	Leu	Ile	Asn	Pro	Gln	Tyr	170	175	180
His	Phe	Ser	Glu	Asp	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Asp	185	190	195
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Ile	Gln	200	205	210
Val	Thr	Arg	Ala	Phe	Ile	Ala	Ala	Arg	Thr	Phe	Val	Gln	Gly	Leu	215	220	225
Thr	Val	Gly	Arg	Glu	Val	Ala	Asn	Arg	Val	Ser	Lys	Val	Ser	Pro	230	235	240
Thr	Pro	Gly	Cys	Ile	Arg	Ala	Leu	Met	Lys	Met	Leu	Tyr	Cys	Pro	245	250	255
Tyr	Cys	Arg	Gly	Leu	Pro	Thr	Val	Arg	Pro	Cys	Asn	Asn	Tyr	Cys	260	265	270
Leu	Asn	Val	Met	Lys	Gly	Cys	Leu	Ala	Asn	Gln	Ala	Asp	Leu	Asp	275	280	285
Thr	Glu	Trp	Asn	Leu	Phe	Ile	Asp	Ala	Met	Leu	Leu	Val	Ala	Glu	290	295	300
Arg	Leu	Glu	Gly	Pro	Phe	Asn	Ile	Glu	Ser	Val	Met	Asp	Pro	Ile	305	310	315
Asp	Val	Lys	Ile	Ser	Glu	Ala	Ile	Met	Asn	Met	Gln	Glu	Asn	Ser	320	325	330
Met	Gln	Val	Ser	Ala	Lys	Val	Phe	Gln	Gly	Cys	Gly	Gln	Pro	Lys	335	340	345
Pro	Ala	Pro	Ala	Leu	Arg	Ser	Ala	Arg	Ser	Ala	Pro	Glu	Asn	Phe	350	355	360
Asn	Thr	Arg	Phe	Arg	Pro	Tyr	Asn	Pro	Glu	Glu	Arg	Pro	Thr	Thr			

365	370	375
Ala Ala Gly Thr Ser Leu Asp Arg Leu	Val Thr Asp Ile Lys Glu	
380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp	Ser Ala Leu Pro Tyr Thr	
395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala	Gly Thr Ser Asn Glu Glu	
410	415	420
Glu Cys Trp Asn Gly His Ser Lys Ala	Arg Tyr Leu Pro Glu Ile	
425	430	435
Met Asn Asp Gly Leu Thr Asn Gln Ile	Asn Asn Pro Glu Val Asp	
440	445	450
Val Asp Ile Thr Arg Pro Asp Thr Phe	Ile Arg Gln Gln Ile Met	
455	460	465
Ala Leu Arg Val Met Thr Asn Lys Leu	Lys Asn Ala Tyr Asn Gly	
470	475	480
Asn Asp Val Asn Phe Gln Asp Thr Ser	Asp Glu Ser Ser Gly Ser	
485	490	495
Gly Ser Gly Ser Gly Cys Met Asp Asp	Val Cys Pro Thr Glu Phe	
500	505	510
Glu Phe Val Thr Thr Glu Ala Pro Ala	Val Asp Pro Asp Arg Arg	
515	520	525
Glu Val Asp Ser Ser Ala Ala Gln Arg	Gly His Ser Leu Leu Ser	
530	535	540
Trp Ser Leu Thr Cys Ile Val Leu Ala	Leu Gln Arg Leu Cys Arg	
545	550	555

- <210> 110
- <211> 21
- <212> DNA
- <213> Artificial Sequence
  
- <220>
- <223> Synthetic oligonucleotide probe
  
- <400> 110
- aagcgtgaca gcgggcacgt c 21
  
- <210> 111
- <211> 24
- <212> DNA
- <213> Artificial Sequence
  
- <220>
- <223> Synthetic oligonucleotide probe
  
- <400> 111

tgcacagtct ctgcagtgcc cagg 24

<210> 112

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgctg 40

<210> 113

<211> 4649

<212> DNA

<213> Homo sapiens

<400> 113

cggacgcgtg ggcggacgcg tgggcaaaag aactcggagt gccaaagcta 50

aataagttag ctgagaaaac gcacgcagtt tgcagcgctt gcgccgggtg 100

cgccaactac gcaaagacca agcgggctcc gcgcggaccg gccgcggggc 150

tagggaccgc gctttggcct tcaggctccc tagcagcggg gaaaaggaat 200

tgctgcccgc agtttctgcg gaggtggagg gagatcagga aacggcttct 250

tcctcacttc gccgcctggt gagtgtcggg gagattggca aacgcctagg 300

aaaggactgg ggaaaatagc cctgggaaag tggagaaggt gatcaggagg 350

ccggtccact acggcagttt atctgtctga tcagagccag acgcgacgcg 400

tccacttcgc agttctttcc aggtgtgggg accgcaggac agacggccga 450

tcccgcgcgc ctccgtacca gcactcccag gagagtcagc ctgcctcccc 500

aacgtcgagg gcgctctggc cacgaaaagt tcctgtccac tgtgattctc 550

aattccttgc ttggtttttt tctccagaga acttttgggt ggagatatta 600

acttttttct tttttttttt ccttggtgga agctgctcta gggagggggg 650

aggaggagga gaaagtgaat tgtgctggag aagagcgagc cctccttggt 700

cttcgcgagt cccatccatt aagccatcac ttctggaaga ttaaagttgt 750

cggacatggt gacagctgag aggagaggag gatttcttgc cagggtggaga 800

gtcttcaccg tctgttgggt gcatgtgtgc gcccgacgcg gcgcggggcg 850

cgtggttctc cgcgtggagt ctcacctggg acctgagtga atggctccca 900

ggggctgtgc ggggcatccg cctccgcctt ctccacaggc ctgtgtctgt 950

cctggaaaga tgctagcaat gggggcgctg gcaggattct ggatcctctg 1000

Sequence = 1000

cctcctcact tatggttacc tgtcctgggg ccaggcctta gaagaggagg 1050  
aagaaggggc cttactagct caagctggag agaaactaga gccagcaca 1100  
acttcacact ccagcccca tctcattttc atcctagcgg atgatcaggg 1150  
atttagagat gtgggttacc acggatctga gattaaaaca cctactcttg 1200  
acaagctcgc tgccgaagga gttaaactgg agaactacta tgtccagcct 1250  
atttgacac catccaggag tcagtttatt actggaaagt atcagatata 1300  
caccggactt caacattcta tcataagacc tacccaaccc aactgtttac 1350  
ctctggacaa tgccacccta cctcagaaac tgaaggaggt tggatattca 1400  
acgcatatgg tcggaaaatg gcacttgggt ttaacagaa aagaatgcat 1450  
gccaccaga agaggatttg ataccttttt tggttccctt ttgggaagtg 1500  
gggattacta tacacactac aaatgtgaca gtctgggat gtgtggctat 1550  
gacttgtatg aaaacgacaa tgctgcctgg gactatgaca atggcatata 1600  
ctccacacag atgtacactc agagagtaca gaaatctta gcttcccata 1650  
acccacaaaa gcctatattt ttatatactg cctatcaagc tgttcattca 1700  
ccactgcaag ctctggcag gtatttcgaa cactaccgat ccattatcaa 1750  
cataaacagg agaagatatg ctgccatgct ttctgctta gatgaagcaa 1800  
tcaacaacgt gacattggct ctaaagactt atggtttcta taacaacagc 1850  
attatcattt actcttcaga taatggtggc cagcctacgg caggaggagg 1900  
taactggcct ctgagaggta gcaaaggaac atattgggaa ggagggatcc 1950  
gggctgtagg ctttgtgcat agcccacttc tgaaaaacaa gggaacagtg 2000  
tgtaaggaac ttgtgcacat cactgactgg taccocactc tcatttcact 2050  
ggctgaagga cagattgatg aggacattca actagatggc tatgatattc 2100  
gggagaccat aagtgagggt cttcgtcac cccgagtaga tattttgcat 2150  
aacattgacc cctatacacc aaggcaaaaa atggctcctg ggcagcaggc 2200  
tatgggatct ggaacactgc aatccagtca gccatcagag tgcagcactg 2250  
gaaattgctt acaggaaatc ctggctacag cgactgggtc cccctcagt 2300  
ctttcagcaa cctgggaccg aaccggtggc acaatgaacg gatcaccttg 2350  
tcaactggca aaagtgtatg gcttttcaac atcacagccg acccatatga 2400  
gaggggtggac ctatctaaca ggtatccagg aatcgtgaag aagctcctac 2450

ggaggctctc acagttcaac aaaactgcag tgccgggtcag gtatccccc 2500  
 aaagacccca gaagtaaccc taggctcaat ggaggggtct ggggaccatg 2550  
 gtataaagag gaaaccaaga aaaagaagcc aagcaaaaat caggctgaga 2600  
 aaaagcaaaa gaaaagcaaa aaaaagaaga agaaacagca gaaagcagtc 2650  
 tcaggtaaac cagcaaattt ggctcgataa tatcgctggc ctaagcgtca 2700  
 ggcttgTTTT catgctgtgc cactccagag acttctgcc cctggccgcc 2750  
 aactgaaaa ctgtctgtct cagtgccaaag gtgctactct tgcaagccac 2800  
 acttagagag agtgagatg tttatttctc tcgtctcttt agaaaacgtg 2850  
 gtgagtcctg agttccactg ctgtgcttca gtcaactgac caaacactgc 2900  
 tttgaattat aggaggagaa caataaccta ccatccgcaa gcatgctaata 2950  
 ttgatggaag ttacagggta gcatgattaa aactaccttt gataaattac 3000  
 agtcaaagat tgtgtcacct caaaggcctt gaagaatata ttttcttggt 3050  
 gaatttttgt atgtctgtca tatgacactt ggggttttta attaatctta 3100  
 ttttatatat ataaatatat gtttcttttc ctgtgaaaag ctgtttttct 3150  
 cacatgtgaa cagcttgcac ctcatcttac catgctgtgag ggaatggcaa 3200  
 ataagaatgt ttgagcacac tgcccacaat gaatgtaact attttctaaa 3250  
 cactttacta gaagaacatt tcagtataaa aaacctaat tatttttaca 3300  
 gaaaaatatt ttgttgTTTT tataaaaagt tatgcaaatg acttttattt 3350  
 ttatttcttg cataccatta gaagaatttt atttcatttc ttcaaattat 3400  
 caagcactgt aatactataa attaatgtaa tactgtgtga attcagacta 3450  
 taaaaaacat cattcagaaa actttataat cgtcattggt caatcaagat 3500  
 tttgaatgta ataagatgaa tatattcctt acaaattact tggaaattca 3550  
 atgtttgtgc agagttgaga caactttatt gtttctatca taaactattt 3600  
 atgtatctta attattaataa tgatttactt tatggcacta gaaaatttac 3650  
 tgtggctttt ctgatctaac ttctagctaa aattgtatca ttggtcctaa 3700  
 aaaataaaaa tctttactaa taggcaattg aaggaatggt ttgctaacaa 3750  
 ccacagtaat ataatatgat ttacagata gatgcttccc cttggctatg 3800  
 acatggagaa agattttccc ataataataa ctaatattta tattaggttg 3850  
 gtgcaaaact agttgcggtt tttccatta aaagtaataa ccttactctt 3900

atacaaagtg gacactgtgg ggagatacag agaaatggaa gatacggatc 3950  
 ctgcctggag taggtaacct tgcttgaaa ccccatatgc aaacgtcatg 4000  
 aggagaatta aaggagtatt atcagtaatg aagtttatca tgggtcatca 4050  
 atgagcatag attggtgtgg atcctgtaga ccctggtgtt ttctttgaag 4100  
 tgccctctcc taatgcagag gccttgaagc ttacagtata cacttgaaaa 4150  
 gtcacagata gctagaatta tgatctttga agttataact gtgatctgaa 4200  
 aatgtgtgtg gtggtatgac agcataccat taaatacatt tacatcacag 4250  
 ctcaaaggac tgtgatataa tccatttata tcacaactca aaggactgtg 4300  
 atataatcca tttatatcac agctcacagt ttctgaaaat gtataaaaaga 4350  
 atctataatc tagtactgaa attactaaat tgggtaagat gatttaaatg 4400  
 attttaattt taacatttta tttctagaat atatggctcc attttatttt 4450  
 atagtgtaaa gttgtatttc cttaaagttg tgtttgtcg acagtatctt 4500  
 ttaaagtgtg cttaaaaata aaggcatatt gttcatgttt aaaaaaaaaa 4550  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4600  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4649

<210> 114  
 <211> 515  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
 Met Ala Pro Arg Gly Cys Ala Gly His Pro Pro Pro Pro Ser Pro  
 1 5 10 15  
 Gln Ala Cys Val Cys Pro Gly Lys Met Leu Ala Met Gly Ala Leu  
 20 25 30  
 Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly Tyr Leu Ser  
 35 40 45  
 Trp Gly Gln Ala Leu Glu Glu Glu Glu Gly Ala Leu Leu Ala  
 50 55 60  
 Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln  
 65 70 75  
 Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp  
 80 85 90  
 Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys  
 95 100 105  
 Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro

110	115	120
Ile Cys Thr Pro Ser Arg Ser Gln Phe	Ile Thr Gly Lys Tyr Gln	
125	130	135
Ile His Thr Gly Leu Gln His Ser Ile	Ile Arg Pro Thr Gln Pro	
140	145	150
Asn Cys Leu Pro Leu Asp Asn Ala Thr	Leu Pro Gln Lys Leu Lys	
155	160	165
Glu Val Gly Tyr Ser Thr His Met Val	Gly Lys Trp His Leu Gly	
170	175	180
Phe Asn Arg Lys Glu Cys Met Pro Thr	Arg Arg Gly Phe Asp Thr	
185	190	195
Phe Phe Gly Ser Leu Leu Gly Ser Gly	Asp Tyr Tyr Thr His Tyr	
200	205	210
Lys Cys Asp Ser Pro Gly Met Cys Gly	Tyr Asp Leu Tyr Glu Asn	
215	220	225
Asp Asn Ala Ala Trp Asp Tyr Asp Asn	Gly Ile Tyr Ser Thr Gln	
230	235	240
Met Tyr Thr Gln Arg Val Gln Gln Ile	Leu Ala Ser His Asn Pro	
245	250	255
Thr Lys Pro Ile Phe Leu Tyr Thr Ala	Tyr Gln Ala Val His Ser	
260	265	270
Pro Leu Gln Ala Pro Gly Arg Tyr Phe	Glu His Tyr Arg Ser Ile	
275	280	285
Ile Asn Ile Asn Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys Leu	
290	295	300
Asp Glu Ala Ile Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr Gly	
305	310	315
Phe Tyr Asn Asn Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly Gly	
320	325	330
Gln Pro Thr Ala Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser Lys	
335	340	345
Gly Thr Tyr Trp Glu Gly Gly Ile Arg	Ala Val Gly Phe Val His	
350	355	360
Ser Pro Leu Leu Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu Val	
365	370	375
His Ile Thr Asp Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu Gly	
380	385	390
Gln Ile Asp Glu Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp Glu	
395	400	405





<400> 117  
gccaccctac ctcagaaact gaaggaggtt ggntattcaa cgcatatggt 50

cgg 53

<210> 118  
<211> 2260  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086  
<223> unknown base

<400> 118  
cggacgcgtg ggtgcgagtg gagcggagga cccgagcggc tgaggagaga 50  
ggaggcggcg gcttagctgc tacggggtcc ggccggcgcc ctcccagggg 100  
gggctcagga ggaggaagga ggacccgtgc gagaatgcct ctgccctgga 150  
gccttgcgct cccgctgctg ctctcctggg tggcagggtg tttcggaac 200  
gcggccagtg caaggcatca cgggttgta gcatcggcac gtcagcctgg 250  
ggtctgtcac tatggaacta aactggcctg ctgctacggc tggagaagaa 300  
acagcaaggg agtctgtgaa gctacatgcg aacctggatg taagtgtgtg 350  
gagtgcgtgg gaccaaaca atgcagatgc tttccaggat acaccgggaa 400  
aacctgcagt caagatgtga atgagtgtgg aatgaaacc cggccatgcc 450  
aacacagatg tgtgaataca cacggaagct acaagtgtt ttgcctcagt 500  
ggccacatgc tcatgccaga tgctacgtgt gtgaactcta ggacatgtgc 550  
catgataaac tgtcagtaca gctgtgaaga cacagaagaa gggccacagt 600  
gcctgtgtcc atcctcagga ctccgcctgg ccccaaatg aagagactgt 650  
ctagatattg atgaatgtgc ctctggtaaa gtcactgtc cctacaatcg 700  
aagatgtgtg aacacatttg gaagctacta ctgcaaatgt cacattgggt 750  
tcgaactgca atatatcagt ggacgatatg actgtataga tataaatgaa 800  
tgtactatgg atagccatac gtgcagccac catgccaatt gttcaatac 850  
ccaagggtcc ttcaagtgt aatgcaagca gggatataaa ggcaatggac 900  
ttcgggtgtc tgctatccct gaaaattctg tgaaggaggt cctcagagca 950  
cctggtacca tcaaagacag aatcaagaag ttgcttgctc aaaaaacag 1000  
catgaaaaag aaggcaaaaa ttaaaaatgt taccacagaa cccaccagga 1050

ctcctacccc taaggtgaac ttgcagccct tcaactatga agagatagtt 1100  
 tccagaggcg ggaactctca tggaggtaaa aaagggaatg aagagaaatg 1150  
 aaagaggggc ttgaggatga gaaaagagaa gagaaagccc tgaagaatga 1200  
 catagaggag cgaagcctgc gaggagatgt gttttccct aaggtgaatg 1250  
 aagcaggatga attcggcctg attctggtcc aaaggaaagc gctaacttcc 1300  
 aaactggaac ataaagattt aaatatctcg gttgactgca gtttcaatca 1350  
 tgggatctgt gactggaac aggatagaga agatgatttt gactggaatc 1400  
 ctgctgatcg agataatgct attggcttct atatggcagt tccggccttg 1450  
 gcaggtcaca agaaagacat tggccgattg aaacttctcc tacctgacct 1500  
 gcaaccccaa agcaacttct gtttgctctt tgattaccgg ctggccggag 1550  
 acaaagtcgg gaaacttcca gtgtttgtga aaaacagtaa caatgccctg 1600  
 gcatgggaga agaccacgag tgaggatgaa aagtgaaga cagggaat 1650  
 tcagttgtat caaggaaactg atgctaccaa aagcatcatt tttgaagcag 1700  
 aacgtggcaa gggcaaaacc ggcgaaatcg cagtggatgg cgtcttgctt 1750  
 gtttcaggct tatgtccaga tagcctttta tctgtggatg actgaatgtt 1800  
 actatcttta tatttgactt tgtatgtcag ttccttggtt tttttgat 1850  
 tgcacatag gacctctggc attttagaat tactagctga aaaattgtaa 1900  
 tgtaccaaca gaaatattat tgtaagatgc ctttcttgta taagatatgc 1950  
 caatatttgc tttaaatata atactactgt atcttctcag tcatttctga 2000  
 atctttccnc attatattat aaaatntgga aangtcagtt tatctcccct 2050  
 cctongtata tctgatttgt atangtangt tgatngcctt ctctctacaa 2100  
 catttctaga aaatagaaaa aaaagcacag agaaatgttt aactgtttga 2150  
 ctcttatgat acttcttgga aactatgaca tcaaagatag acttttgcct 2200  
 aagtggctta gctgggtctt tcatagccaa acttgatat ttaattcttt 2250  
 gtaataataa 2260

<210> 119  
 <211> 338  
 <212> PRT  
 <213> Homo sapiens

<400> 119  
 Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu Ser Trp  
 1 5 10 15



	305	310	315
Phe Asn Tyr Glu	Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly		
	320	325	330
Gly Lys Lys Gly	Asn Glu Glu Lys		
	335		

<210> 120  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 120  
 cctcagtggc cacatgctca tg 22

<210> 121  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 121  
 ggctgcacgt atggctatcc atag 24

<210> 122  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 122  
 gataaactgt cagtacagct gtgaagacac agaagaagg ccacagtgcc 50

<210> 123  
 <211> 1199  
 <212> DNA  
 <213> Homo sapiens

<400> 123  
 gggagctgct gctgtggctg ctgggtgctgt gcgcgtgct cctgctcttg 50  
 gtgcagctgc tgcgcttcct gagggctgac ggcgacctga cgctactatg 100  
 ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatggtgg 150  
 tgtgggtgac tggagcctcg agtggattg gtgaggagct ggcttaccag 200  
 ttgtctaaac taggagtttc tcttgctgctg tcagccagaa gagtgcata 250  
 gctggaaagg gtgaaaagaa gatgcctaga gaatggcaat ttaaaagaaa 300

aagatatact tgttttgccc cttgacctga ccgacctgg ttcccatgaa 350  
gcggctacca aagctgttct ccaggagttt ggtagaatcg acattctggt 400  
caacaatggt ggaatgtccc agcgttctct gtgcatggat accagcttgg 450  
atgtctacag aaagctaata gagcttaact acttagggac ggtgtccttg 500  
acaaaatgtg ttctgcctca catgatcgag aggaagcaag gaaagattgt 550  
tactgtgaat agcatcctgg gtatcatatc tgtacctctt tccattggat 600  
actgtgctag caagcatgct ctccggggtt tttttaatgg ccttcgaaca 650  
gaacttgcca catacccagg tataatagtt tctaacattt gcccaggacc 700  
tgtgcaatca aatattgtgg agaattccct agctggagaa gtcacaaaga 750  
ctataggcaa taatggagac cagtcccaca agatgacaac cagtcgttgt 800  
gtgcggctga tgttaatcag catggccaat gatttgaaag aagtttggat 850  
ctcagaacaa cctttcttgt tagtaacata tttgtggcaa tacatgcaa 900  
cctgggcctg gtggataacc aacaagatgg ggaagaaaag gattgagaac 950  
tttaagagtg gtgtggatgc agactcttct tattttaaaa tctttaagac 1000  
aaaacatgac tgaaaagagc acctgtactt ttcaagccac tggagggaga 1050  
aatggaaaac atgaaaacag caatcttctt atgcttctga ataatcaaag 1100  
actaatttgt gattttactt tttaatagat atgactttgc ttccaacatg 1150  
gaatgaaata aaaaataaat aataaaagat tgccatgaat cttgcaaaa 1199

<210> 124  
<211> 289  
<212> PRT  
<213> Homo sapiens

<400> 124  
Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu  
1 5 10 15  
Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser  
20 25 30  
Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu  
35 40 45  
Glu Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu  
50 55 60  
Asp Leu Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val  
65 70 75  
Leu Gln Glu Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly

	80		85		90
Met Ser Gln Arg	Ser Leu Cys Met Asp	Thr Ser Leu Asp Val Tyr			
	95	100			105
Arg Lys Leu Ile	Glu Leu Asn Tyr Leu	Gly Thr Val Ser Leu Thr			
	110	115			120
Lys Cys Val Leu	Pro His Met Ile Glu	Arg Lys Gln Gly Lys Ile			
	125	130			135
Val Thr Val Asn	Ser Ile Leu Gly Ile	Ile Ser Val Pro Leu Ser			
	140	145			150
Ile Gly Tyr Cys	Ala Ser Lys His Ala	Leu Arg Gly Phe Phe Asn			
	155	160			165
Gly Leu Arg Thr	Glu Leu Ala Thr Tyr	Pro Gly Ile Ile Val Ser			
	170	175			180
Asn Ile Cys Pro	Gly Pro Val Gln Ser	Asn Ile Val Glu Asn Ser			
	185	190			195
Leu Ala Gly Glu	Val Thr Lys Thr Ile	Gly Asn Asn Gly Asp Gln			
	200	205			210
Ser His Lys Met	Thr Thr Ser Arg Cys	Val Arg Leu Met Leu Ile			
	215	220			225
Ser Met Ala Asn	Asp Leu Lys Glu Val	Trp Ile Ser Glu Gln Pro			
	230	235			240
Phe Leu Leu Val	Thr Tyr Leu Trp Gln	Tyr Met Pro Thr Trp Ala			
	245	250			255
Trp Trp Ile Thr	Asn Lys Met Gly Lys	Lys Arg Ile Glu Asn Phe			
	260	265			270
Lys Ser Gly Val	Asp Ala Asp Ser Ser	Tyr Phe Lys Ile Phe Lys			
	275	280			285

Thr Lys His Asp

<210> 125  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 125  
 gcaatgaact gggagctgc 19

<210> 126  
 <211> 19  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

ctttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggt atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gagtggcagg gacgacgcc agaag 46

<210> 131

<211> 2365

<212> DNA

<213> Homo sapiens

<400> 131



gcgacgtggg caccgccatc agctgttcgc gcgtttctc ctccaggtgg 50  
 ggacgggggt tgggctggt ggagcatgtg ctgggacagg acagcatcct 100  
 caatcaatcc aacagcatat tcggttgcat cttctacaca ctacagctat 150  
 tgttaggttg cctgcggaca cgctgggcct ctgtcctgat gctgctgagc 200  
 tccctggtgt ctctcgtgg ttctgtctac ctggcctgga tcctgttctt 250  
 cgtgctctat gatttctgca ttgtttgtat caccacctat gctatcaacg 300  
 tgagcctgat gtggctcagt ttccggaagg tccaagaacc ccagggaag 350  
 gctaagaggc actgagccct caacccaagc caggctgacc tcctctgctt 400  
 tgctttggtc ttcaagccgc tcagcgtgcc tgtggacagc gtggccccgg 450  
 ccccccaag cctcaggagg gcaacacagt ccctggcgag tggccctggc 500  
 aggccagtgt gaggaggcaa ggagcccaca tctgcagcgg ctccctggtg 550  
 gcagacacct gggctctcac tgctgccac tgctttgaaa aggagcagc 600  
 aacagaactg aattcctggt cagtggctct gggttctctg cagcgtgagg 650  
 gactcagccc tggggccgaa gaggtggggg tggtgccct gcagttgcc 700  
 agggcctata accactacag ccagggtca gacctggccc tgctgcagct 750  
 cgcccacccc acgaccaca caccctctg cctgcccag cccgccatc 800  
 gcttccctt tggagcctcc tgctgggcca ctggctggga tcaggacacc 850  
 agtgatgctc ctgggacct acgcaatctg cgctgcgtc tcctcagctg 900  
 cccacatgt aactgtatct acaaccagct gcaccagcga cacctgtcca 950  
 acccgggccg gcctgggatg ctatgtggg gccccagcc tggggtgcag 1000  
 ggccctgtc agggagattc cgggggccct gtgtgtgcc tcgagcctga 1050  
 cggacactgg gttcaggctg gcatcatcag ctttgcata agctgtgcc 1100  
 aggaggacgc tcctgtgctg ctgaccaaca cagctgctca cagttcctgg 1150  
 ctgcaggctc gaggtcagg ggagctttc ctggcccaga gccagagac 1200  
 ccggagatg agtgatgagg acagctgtgt agcctgtgga tccttgagga 1250  
 cagcaggtcc ccaggcagga gcacctccc catggccctg ggaggccagg 1300  
 ctgatgcacc agggacagct ggcctgtggc ggagccctg tgtcagagga 1350  
 ggcggtgcta actgtgccc actgcttcat tgggcgccag gccccagagg 1400  
 aatggagcgt agggctggg accagaccg aggagtggg cctgaagcag 1450

ctcatcctgc atggagccta caccacacct gaggggggct acgacatggc 1500  
cctcctgctg ctggcccagc ctgtgacact gggagccagc ctgcggcccc 1550  
tgtcctgcc ctatcctgac caccacctgc ctgatgggga gcgtggctgg 1600  
gttctgggac gggcccggcc aggagcaggc atcagctccc tccagacagt 1650  
gcccgtagacc ctctggggc ctagggcctg cagccggctg catgcagctc 1700  
ctgggggtga tggcagccct attctgccgg ggatggtgtg taccagtgt 1750  
gtgggtgagc tgcccagctg tgagggcctg tctggggcac cactggtgca 1800  
tgaggtgagg ggcacatggt tcctggccgg gctgcacagc ttcggagatg 1850  
cttgccaagg ccccgccagg ccggcgggtct tcaccgcgct ccctgcctat 1900  
gaggactggg tcagcagttt ggactggcag gtctacttcg ccgaggaacc 1950  
agagcccag gctgagcctg gaagctgcct ggccaacata agccaaccaa 2000  
ccagctgctg acaggggacc tggccattct caggacaaga gaatgcaggc 2050  
aggcaaatgg cattactgcc cctgtcctcc ccaccctgtc atgtgtgatt 2100  
ccaggcacca gggcaggccc agaagcccag cagctgtggg aaggaacctg 2150  
cctggggcca caggtgccc ctccccaccc tgcaggacag ggggtgtctgt 2200  
ggacactccc acaccaact ctgctaccaa gcaggcgtct cagctttcct 2250  
cctcctttac tctttcagat acaatcacgc cagccacgtt gttttgaaa 2300  
tttctttttt tggggggcag cagttttcct ttttttaaac ttaaataaat 2350  
tgttacaaaa taaaa 2365

<210> 132  
<211> 571  
<212> PRT  
<213> Homo sapiens

<400> 132  
Met Leu Leu Ser Ser Leu Val Ser Leu Ala Gly Ser Val Tyr Leu  
1 5 10 15  
Ala Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe Cys Ile Val Cys  
20 25 30  
Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe  
35 40 45  
Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn  
50 55 60  
Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln  
65 70 75

Gly Ala His Ile Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val  
 80 85 90  
 Leu Thr Ala Ala His Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu  
 95 100 105  
 Asn Ser Trp Ser Val Val Leu Gly Ser Leu Gln Arg Glu Gly Leu  
 110 115 120  
 Ser Pro Gly Ala Glu Glu Val Gly Val Ala Ala Leu Gln Leu Pro  
 125 130 135  
 Arg Ala Tyr Asn His Tyr Ser Gln Gly Ser Asp Leu Ala Leu Leu  
 140 145 150  
 Gln Leu Ala His Pro Thr Thr His Thr Pro Leu Cys Leu Pro Gln  
 155 160 165  
 Pro Ala His Arg Phe Pro Phe Gly Ala Ser Cys Trp Ala Thr Gly  
 170 175 180  
 Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly Thr Leu Arg Asn Leu  
 185 190 195  
 Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn Cys Ile Tyr Asn  
 200 205 210  
 Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg Pro Gly Met  
 215 220 225  
 Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys Gln Gly  
 230 235 240  
 Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His Trp  
 245 250 255  
 Val Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu  
 260 265 270  
 Asp Ala Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp  
 275 280 285  
 Leu Gln Ala Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro  
 290 295 300  
 Glu Thr Pro Glu Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly  
 305 310 315  
 Ser Leu Arg Thr Ala Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp  
 320 325 330  
 Pro Trp Glu Ala Arg Leu Met His Gln Gly Gln Leu Ala Cys Gly  
 335 340 345  
 Gly Ala Leu Val Ser Glu Glu Ala Val Leu Thr Ala Ala His Cys  
 350 355 360  
 Phe Ile Gly Arg Gln Ala Pro Glu Glu Trp Ser Val Gly Leu Gly

	365		370		375
Thr Arg Pro Glu	Glu Trp Gly Leu Lys	Gln Leu Ile Leu His	Gly		
	380	385	390		
Ala Tyr Thr His	Pro Glu Gly Gly Tyr	Asp Met Ala Leu Leu	Leu		
	395	400	405		
Leu Ala Gln Pro	Val Thr Leu Gly Ala	Ser Leu Arg Pro Leu	Cys		
	410	415	420		
Leu Pro Tyr Pro	Asp His His Leu Pro	Asp Gly Glu Arg Gly	Trp		
	425	430	435		
Val Leu Gly Arg	Ala Arg Pro Gly Ala	Gly Ile Ser Ser Leu	Gln		
	440	445	450		
Thr Val Pro Val	Thr Leu Leu Gly Pro	Arg Ala Cys Ser Arg	Leu		
	455	460	465		
His Ala Ala Pro	Gly Gly Asp Gly Ser	Pro Ile Leu Pro Gly	Met		
	470	475	480		
Val Cys Thr Ser	Ala Val Gly Glu Leu	Pro Ser Cys Glu Gly	Leu		
	485	490	495		
Ser Gly Ala Pro	Leu Val His Glu Val	Arg Gly Thr Trp Phe	Leu		
	500	505	510		
Ala Gly Leu His	Ser Phe Gly Asp Ala	Cys Gln Gly Pro Ala	Arg		
	515	520	525		
Pro Ala Val Phe	Thr Ala Leu Pro Ala	Tyr Glu Asp Trp Val	Ser		
	530	535	540		
Ser Leu Asp Trp	Gln Val Tyr Phe Ala	Glu Glu Pro Glu Pro	Glu		
	545	550	555		
Ala Glu Pro Gly	Ser Cys Leu Ala Asn	Ile Ser Gln Pro Thr	Ser		
	560	565	570		

Cys

<210> 133  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 133  
 cctgtgctgt gcctcgagcc tgac 24

<210> 134  
 <211> 24  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggccgccc ccggcccca ttcgggccgg gcctcgctgc ggcggcgact 50

gagccaggct gggccgcgtc cctgagtccc agagtcggcg cggcgcggca 100

ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctcacaggaa 150

gatgctgcgt cggcggggca gccctggcat ggggtgtcat gtgggtgcag 200

ccctgggagc actgtggttc tgcctcacag gagccctgga ggtccaggtc 250

cctgaagacc cagtgtgtggc actggtgggc accgatgcca cctgtgctg 300

ctccttctcc cctgagcctg gcttcagcct ggacacagtc aacctcatct 350

ggcagctgac agatacaaaa cagctggtgc acagctttgc tgagggccag 400

gaccagggca gcgcctatgc caaccgcacg gccctcttcc cggacctgct 450

ggcacagggc aacgcattccc tgaggctgca gcgcgtgcgt gtggcggacg 500

agggcagctt cacctgcttc gtgagcatcc gggatttcgg cagcgtgcc 550

gtcagcctgc aggtggccgc tccctactcg aagcccagca tgaccctgga 600

gccaacaag gacctgcggc caggggacac ggtgaccatc acgtgctcca 650

gctaccaggc ctaccctgag gctgaggtgt tctggcagga tgggcagggt 700

gtgcccctga ctggcaacgt gaccacgtcg cagatggcca acgagcaggg 750

cttgtttgat gtgcacagcg tcctgcgggt ggtgctgggt gcgaatggca 800

cctacagctg cctggtgcgc aaccccgctg tgcagcagga tgcgcacrgc 850



1	5	10	15
Ala Ala Leu Gly	Ala Leu Trp Phe Cys	Leu Thr Gly Ala Leu	Glu 30
20		25	
Val Gln Val Pro Glu Asp	Pro Val Val Ala Leu Val Gly Thr	Asp	45
35		40	
Ala Thr Leu Cys Cys Ser Phe Ser Pro	Glu Pro Gly Phe Ser	Leu	60
50		55	
Ala Gln Leu Asn Leu Ile Trp Gln Leu	Thr Asp Thr Lys Gln Leu		75
65		70	
Val His Ser Phe Ala Glu Gly Gln Asp	Gln Gly Ser Ala Tyr Ala		90
80		85	
Asn Arg Thr Ala Leu Phe Pro Asp Leu	Leu Ala Gln Gly Asn Ala		105
95		100	
Ser Leu Arg Leu Gln Arg Val Arg Val	Ala Asp Glu Gly Ser Phe		120
110		115	
Thr Cys Phe Val Ser Ile Arg Asp Phe	Gly Ser Ala Ala Val Ser		135
125		130	
Leu Gln Val Ala Ala Pro Tyr Ser Lys	Pro Ser Met Thr Leu Glu		150
140		145	
Pro Asn Lys Asp Leu Arg Pro Gly Asp	Thr Val Thr Ile Thr Cys		165
155		160	
Ser Ser Tyr Gln Gly Tyr Pro Glu Ala	Glu Val Phe Trp Gln Asp		180
170		175	
Gly Gln Gly Val Pro Leu Thr Gly Asn	Val Thr Thr Ser Gln Met		195
185		190	
Ala Asn Glu Gln Gly Leu Phe Asp Val	His Ser Val Leu Arg Val		210
200		205	
Val Leu Gly Ala Asn Gly Thr Tyr Ser	Cys Leu Val Arg Asn Pro		225
215		220	
Val Leu Gln Gln Asp Ala His Xaa Ser	Val Thr Ile Thr Gly Gln		240
230		235	
Pro Met Thr Phe Pro Pro Glu Ala Leu	Trp Val Thr Val Gly Leu		255
245		250	
Ser Val Cys Leu Ile Ala Leu Leu Val	Ala Leu Ala Phe Val Cys		270
260		265	
Trp Arg Lys Ile Lys Gln Ser Cys Glu	Glu Glu Asn Ala Gly Ala		285
275		280	
Glu Asp Gln Asp Gly Glu Gly Glu Gly	Ser Lys Thr Ala Leu Gln		300
290		295	

Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile  
 305 310 315

Ala

<210> 138  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 138  
 ctggcacagc tcaacctcat ctgg 24

<210> 139  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 139  
 gctgtctgtc tgtctcattg 20

<210> 140  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 140  
 ggacacagta tactgaccac 20

<210> 141  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 141  
 tgcgaaccag gcagctgtaa gtgc 24

<210> 142  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe



<400> 142  
tggaagaaga ggggtggtgat gtgg 24

<210> 143  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 143  
cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144  
<211> 2336  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1620, 1673  
<223> unknown base

<400> 144  
ttcgtgaccc ttgagaaaag agttggtggt aaatgtgcc cgtcttctaa 50  
gaagggggag tcttgaactt gtctgaagcc cttgtccgta agccttgaac 100  
tacgtttctta aatctatgaa gtcgaggac ctttcgctgc tttttaggg 150  
acttctttcc ttgcttcagc aacatgaggc ttttcttggtg gaacgcggtc 200  
ttgactctgt togtcacttc tttgattggg gctttgatcc ctgaaccaga 250  
agtgaataatt gaagttctcc agaagccatt catctgccat cgcaagacca 300  
aaggagggga tttgatgttg gtccactatg aaggctactt agaaaaggac 350  
ggctccttat ttcactccac tcacaaacat aacaatggtc agcccatttg 400  
gtttaccctg ggcctcctgg aggctctcaa aggttgggac cagggttgga 450  
aaggaatgtg tgtaggagag aagagaaagc tcatcattcc tctgtctctg 500  
ggctatggaa aagaaggaaa aggtaaaatt ccccagaaa gtacactgat 550  
atttaatatatt gatctcctgg agattcgaaa tggaccaaga tcccatgaat 600  
cattccaaga aatggatctt aatgatgact ggaaactctc taaagatgag 650  
gttaaagcat atttaaagaa ggagtttgaa aaacatggtg cgggtggtgaa 700  
tgaaagtcatt catgatgctt tgggtggagga tatttttgat aaagaagatg 750  
aagacaaaga tgggtttata tctgccagag aatttacata taaacacgat 800  
gagttataga gatacatcta cccttttaaat atagcactca tctttcaaga 850

gagggcagtc atctttaag aacattttat tttatacaa tgttctttct 900  
tgctttgttt tttattttta tatatttttt ctgactocta tttaaagaac 950  
cccttaggtt tctaagtacc catttctttc tgataagtta ttggaagaa 1000  
aaagctaatt ggtctttgaa tagaagactt ctggacaatt tttcactttc 1050  
acagatatga agctttgttt tacttttctca cttataaatt taaaatgttg 1100  
caactgggaa tataaccacga catgagacca gggtatagca caaattagca 1150  
ccctatattt ctgcttcctt ctattttctc caagttagag gtcaacattt 1200  
gaaaagcctt ttgcaatagc ccaaggcttg ctattttcat gttataatga 1250  
aatagtttat gtgtaactgg ctctgagtct ctgcttgagg accagaggaa 1300  
aatggttggt ggacctgact tgttaatggc tactgcttta ctaaggagat 1350  
gtgcaatgct gaagttagaa acaaggtaa tagccaggca tggtggtca 1400  
tgctgtaat ccagcactt tgggaggctg aggcgggagg atcacctgag 1450  
gttgggagtt cgagaccagc ctgaccaaca cggagaaacc ctatctctac 1500  
taaaaataca aagtagcccg gcgtggtgat gcgtgcctgt aatcccagct 1550  
accaggaag gctgaggcgg cagaatcact tgaacccgag gccgaggttg 1600  
cggtaagccg agatcacctn cagcctggac actctgtctc gaaaaaagaa 1650  
aagaacacgg ttaataccat atnaatatgt atgcattgag acatgctacc 1700  
taggacttaa gctgatgaag cttggctcct agtgattggt ggcctattat 1750  
gataaatagg acaaatcatt tatgtgtgag tttctttgta ataaaatgta 1800  
tcaatatggt atagatgagg tagaaagtta tatttatatt caatatttac 1850  
ttcttaaggc tagcgaata tccttcctgg ttctttaatg ggtagtctat 1900  
agtatattat actacaataa cattgtatca taagataaag tagtaaacca 1950  
gtctacattt tcccatttct gtctcatcaa aaactgaagt tagctgggtg 2000  
tggtggtca tgctgtaat ccagcactt tgggggcaa ggagggtgga 2050  
tcacttgaga tcaggagttc aagaccagcc tggccaacat ggtgaaacct 2100  
tgtctctact aaaaatacaa aaattagcca ggcgtggtgg tgcacacctg 2150  
tagtcccagc tactcgggag gctgagacag gagatttgct tgaacccggg 2200  
aggcggaggt tgcagtgagc caagattgtg ccaactgcact ccagcctggg 2250  
tgacagagca agactccatc tcaaaaaaaa aaaaaagaag cagacctaca 2300

gcagctacta ttgaataaat acctatcctg gatttt 2336

<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

Met Arg Leu Phe Leu Trp Asn Ala Val Leu Thr Leu Phe Val Thr  
1 5 10 15

Ser Leu Ile Gly Ala Leu Ile Pro Glu Pro Glu Val Lys Ile Glu  
20 25 30

Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly  
35 40 45

Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly  
50 55 60

Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile  
65 70 75

Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln  
80 85 90

Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile  
95 100 105

Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro  
110 115 120

Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg  
125 130 135

Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn  
140 145 150

Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys  
155 160 165

Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His  
170 175 180

Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys  
185 190 195

Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu  
200 205 210

Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 146  
ctttccttgc ttcagcaaca tgaggc 26

<210> 147  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 147  
gcccagagca ggaggaatga tgagc 25

<210> 148  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 148  
gtggaacgcg gtcttgactc tgcttcacac ttctttgatt ggggctttg 49

<210> 149  
<211> 2196  
<212> DNA  
<213> Homo sapiens

<400> 149  
aataaagctt ccttaatggt gtatatgtct ttgaagtaca tccgtgcatt 50  
tttttttagc atccaaccat tctcccttg tagttctgc cccctcaaatt 100  
caccctctcc cgtagccac ccgactaaca tctcagctc tgaaaatgca 150  
cagagatgcc tggtacctc gccctgcctt cagcctcacg gggctcagtc 200  
tctttttctc ttgggtgccca ccaggacgga gcatggaggt cacagtacct 250  
gccaccctca acgtctcaa tggctctgac gccgcctgc cctgcacctt 300  
caactcctgc tacacagtga accacaaaca gttctccctg aactggactt 350  
accaggagtg caacaactgc tctgaggaga tggtcctcca gttccgcatg 400  
aagatcatta acctgaagct ggagcggttt caagaccgcg tggagttctc 450  
agggaacccc agcaagtacg atgtgtcggg gatgctgaga aacgtgcagc 500  
cggaggatga ggggatttac aactgctaca tcatgaaccc ccctgaccgc 550  
caccgtggcc atggcaagat ccatctgcag gtcctcatgg aagagcccc 600



cgtgtgcctg taatcccagc tatttgggag gctgaggcag gagaatcgct 2100  
 tgagcccggg aagcagaggt tgcaagtgaac tgagatagtg atagtccac 2150  
 tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150  
 <211> 215  
 <212> PRT  
 <213> Homo sapiens

<400> 150  
 Met His Arg Asp Ala Trp Leu Pro Arg Pro Ala Phe Ser Leu Thr  
 1 5 10 15  
 Gly Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met  
 20 25 30  
 Glu Val Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp  
 35 40 45  
 Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His  
 50 55 60  
 Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys  
 65 70 75  
 Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu  
 80 85 90  
 Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro  
 95 100 105  
 Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu  
 110 115 120  
 Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg  
 125 130 135  
 His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu  
 140 145 150  
 Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser  
 155 160 165  
 Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val  
 170 175 180  
 Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp  
 185 190 195  
 Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro  
 200 205 210  
 Asp Asp Gly Ala Lys  
 215

<210> 151

<211> 524  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 103, 233  
<223> unknown base

<400> 151  
gttgatatg.tcctgaagta catccgtgca ttttttttag catccaacca 50  
tcctcccttg tagttctcgc cccctcaaat caccttctcc cttagccac 100  
ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150  
gccctgcctt cagcctcacg gggctcagtc tttttttctc tttggtgcc 200  
ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtctc 250  
aatggctctg acgcccgcct gccctgcct tcaactcctg ctacacagtg 300  
aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350  
ctctgaggag atgttctcc agttccgcat gaagatcatt aacctgaagc 400  
tgagcgggt tcaagaccgc gtggagttct cagggaaccc cagcaagtac 450  
gatgtgtcgg tgatgtgag aaacgtgcag ccggaggatg aggggattta 500  
caactgctac atcatgaacc cccc 524

<210> 152  
<211> 368  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 56, 123  
<223> unknown base

<400> 152  
tcacggggct catctctttt tctctttggt gccaccagg acggagcatg 50  
gaggtncaca tacctgccac cctcaacgtc ctcaatggct ttgacgccg 100  
cctgccctgc accttcaact cngctacac agtgaaccac aaacagttct 150  
ccctgaactg gatttaccag gagtgaaca actggctctg aggagatgtt 200  
cctccagttc cgcgatggaa gatcatttaa cctgaaagct ggaagcgggt 250  
ttcaagaacc gcgtggaagt ttctcaggga accccagcaa gtacgatgtg 300  
tcggtgatgc tgagaaacgt gcagccggag gatgagggga ttacaactg 350  
ctacatcatg aaccccc 368

<210> 153  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 153  
 acggagcatg gaggtccaca gtac 24

<210> 154  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 154  
 gcacgtttct cagcatcacc gac 23

<210> 155  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 155  
 cgctgcccct gcaccttcaa ctctgctac acagtgaacc acaaacagtt 50

<210> 156  
 <211> 2680  
 <212> DNA  
 <213> Homo sapiens

<400> 156  
 tgcggcgacc gtcgtacacc atgggectcc acctccgccc ctaccgtgtg 50  
 gggctgctcc cggatggcct cctgttcttc ttgctgctgc taatgctgct 100  
 cgcggaccca gcgctcccg cggacgtca cccccagtg gtgctggtcc 150  
 ctggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagtg 200  
 gtgcactacc tctgctcaa gaagaccgaa agctacttca caatctggct 250  
 gaacctggaa ctgctgctgc ctgtcatcat tgactgctgg attgacaata 300  
 tcaggctggg ttacaacaaa acatccaggg ccaccagtt tctgatggg 350  
 gtggatgtac gtgtccctgg ctttgggaag accttctcac tggagttcct 400  
 ggacccagc aaaagcagcg tgggttcta tttccacacc atggtggaga 450  
 gccttgtggg ctggggctac acacggggtg aggatgtccg aggggctccc 500



tatgactggc gccgagcccc aatgaaaac gggccctact tcctggccct 550  
 ccgcgagatg atcgaggaga tgtaccagct gtatgggggc cccgtggtgc 600  
 tggttgcccc cagtatgggc aacatgtaca cgctctactt tctgcagcgg 650  
 cagccgcagg cctggaagga caagtatatc cgggccttcg tgtcactggg 700  
 tgcgccctgg gggggcgtgg ccaagaccct gcgcgtctg gcttcaggag 750  
 acaacaaccg gatccagtc atcgggcccc tgaagatccg ggagcagcag 800  
 cggtcagctg tctccaccag ctggctgctg ccctacaact acacatggtc 850  
 acctgagaag gtgttcgtgc agacaccac aatcaactac aactgcggg 900  
 actaccgcaa gttcttcag gacatcggt ttgaagatgg ctggctcatg 950  
 cggcaggaca cagaagggt ggtggaagcc acgatgccac ctggcgtgca 1000  
 gctgcactgc ctctatgta ctggcgtccc cacaccagac tccttctact 1050  
 atgagagctt ccctgaccgt gaccctaaaa tctgctttgg tgacggcgat 1100  
 ggtactgtga acttgaagag tgccctgcag tgccaggcct ggcagagccg 1150  
 ccaggagcac caagtgttg tgcaggagct gccaggcagc gagcacatcg 1200  
 agatgctggc caacgccacc accctggcct atctgaaacg tgtgctcctt 1250  
 gggccctgac tcctgtgcca caggactcct gtggctcggc cgtggacctg 1300  
 ctgttgccct ctggggctgt catggccac gcgttttgca aagtttgtga 1350  
 ctcaccattc aaggccccga gtcttgact gtgaagcacc tgccatggg 1400  
 aagtgtgtt tggtatcctt tctctgtggc agtgaagaag gaagaaatga 1450  
 gagtctagac tcaagggaca ctggatggca agaagctgc tgatggtgga 1500  
 actgctgtga ccttaggact ggctccacag ggtggactgg ctgggcccctg 1550  
 gtccagtcct ctgcctgggg ccattgtgct ccctattcct gtgggctttt 1600  
 catacttgcc tactggggcc tggccccgca gccttcctat gagggatgtt 1650  
 actgggctgt ggtcctgtac ccagaggtcc cagggatcgg ctccctggccc 1700  
 ctcgggtgac ccttcccaca caccagccac agataggcct gccactggtc 1750  
 atgggtagct agagctgctg gcttcctgt ggcttagctg gtggccagcc 1800  
 tgactggctt cctgggcgag cctagtagct cctgcaggca ggggcagttt 1850  
 gttgcgttct tegtgttcc caggccctgg gacatctcac tccactccta 1900  
 cctcccttac caccaggagc attcaagctc tggattgggc agcagatgtg 1950

cccccagtcc cgcaggctgt gttccagggg ccctgatttc ctggatgtg 2000  
 ctattggccc caggactgaa gctgcctccc ttcaccctgg gactgtggtt 2050  
 ccaaggatga gagcaggggt tggagccatg gccttctggg aacctatgga 2100  
 gaaaggggaat ccaaggaagc agccaaggct gctcgagct tccctgagct 2150  
 gcacctcttg ctaacccac catcacactg ccaccctgcc ctagggtctc 2200  
 actagtacca agtgggtcag cacagggtg aggatggggc tcctatccac 2250  
 cctggccagc acccagctta gtgctgggac tagccagaa acttgaatgg 2300  
 gacctgaga gagccagggg tccctgagg ccccccagg ggctttctgt 2350  
 ctgccccagg gtgctccatg gatctccctg tggcagcagg catggagagt 2400  
 cagggtgcc ttcattggcag taggtcttaa gtgggtgact ggccacaggc 2450  
 cgagaaaagg gtacagcctc taggtggggg tcccaaagac gccttcaggc 2500  
 tggactgagc tgctctcca cagggttct gtgcagctgg attttctctg 2550  
 ttgcatacat gcctggcatc tgtctccct gtgtcctgag tggcccaca 2600  
 tggggctctg agcaggctgt atctggattc tggcaataaa agtactctg 2650  
 atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157  
 <211> 412  
 <212> PRT  
 <213> Artificial

<400> 157  
 Met Gly Leu His Leu Arg Pro Tyr Arg Val Gly Leu Leu Pro Asp  
 1 5 10 15  
 Gly Leu Leu Phe Leu Leu Leu Leu Met Leu Leu Ala Asp Pro  
 20 25 30  
 Ala Leu Pro Ala Gly Arg His Pro Pro Val Val Leu Val Pro Gly  
 35 40 45  
 Asp Leu Gly Asn Gln Leu Glu Ala Lys Leu Asp Lys Pro Thr Val  
 50 55 60  
 Val His Tyr Leu Cys Ser Lys Lys Thr Glu Ser Tyr Phe Thr Ile  
 65 70 75  
 Trp Leu Asn Leu Glu Leu Leu Leu Pro Val Ile Ile Asp Cys Trp  
 80 85 90  
 Ile Asp Asn Ile Arg Leu Val Tyr Asn Lys Thr Ser Arg Ala Thr  
 95 100 105  
 Gln Phe Pro Asp Gly Val Asp Val Arg Val Pro Gly Phe Gly Lys

	110	115	120
Thr Phe Ser Leu	Glu Phe Leu Asp Pro	Ser Lys Ser Ser Val Gly	135
	125	130	
Ser Tyr Phe His	Thr Met Val Glu Ser	Leu Val Gly Trp Gly Tyr	150
	140	145	
Thr Arg Gly Glu	Asp Val Arg Gly Ala	Pro Tyr Asp Trp Arg Arg	165
	155	160	
Ala Pro Asn Glu	Asn Gly Pro Tyr Phe	Leu Ala Leu Arg Glu Met	180
	170	175	
Ile Glu Glu Met	Tyr Gln Leu Tyr Gly	Gly Pro Val Val Leu Val	195
	185	190	
Ala His Ser Met	Gly Asn Met Tyr Thr	Leu Tyr Phe Leu Gln Arg	210
	200	205	
Gln Pro Gln Ala	Trp Lys Asp Lys Tyr	Ile Arg Ala Phe Val Ser	225
	215	220	
Leu Gly Ala Pro	Trp Gly Gly Val Ala	Lys Thr Leu Arg Val Leu	240
	230	235	
Ala Ser Gly Asp	Asn Asn Arg Ile Pro	Val Ile Gly Pro Leu Lys	255
	245	250	
Ile Arg Glu Gln	Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu Leu	270
	260	265	
Pro Tyr Asn Tyr	Thr Trp Ser Pro Glu	Lys Val Phe Val Gln Thr	285
	275	280	
Pro Thr Ile Asn	Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe Gln	300
	290	295	
Asp Ile Gly Phe	Glu Asp Gly Trp Leu	Met Arg Gln Asp Thr Glu	315
	305	310	
Gly Leu Val Glu	Ala Thr Met Pro Pro	Gly Val Gln Leu His Cys	330
	320	325	
Leu Tyr Gly Thr	Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr Glu	345
	335	340	
Ser Phe Pro Asp	Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly Asp	360
	350	355	
Gly Thr Val Asn	Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp Gln	375
	365	370	
Ser Arg Gln Glu	His Gln Val Leu Leu	Gln Glu Leu Pro Gly Ser	390
	380	385	
Glu His Ile Glu	Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr Leu	405
	395	400	

Lys Arg Val Leu Leu Gly Pro  
410

<210> 158  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 158  
ctggggctac acacggggtg agg 23

<210> 159  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 159  
ggtgccgctg cagaaagtag agcg 24

<210> 160  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 160  
gccccaaatg aaaacgggcc ctacttcctg gccctccgcg agatg 45

<210> 161  
<211> 1512  
<212> DNA  
<213> Homo sapiens

<400> 161  
cgacgcgctg ggcggacgcg tggggcggcg gcagcggcg cgacggcgac 50  
atggagagcg gggcctacgg cgcgccaag gcggcggt ccttcgacct 100  
gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150  
tcttcgcctt gatcgtgttc tctgcacatc atggtgaggg ctacagcaat 200  
gccacgagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250  
ctgccgctat ggcagtgcc tgggggtgct ggccttcctg gcctcggcct 300  
tcttcttggg ggtcgacgcg tatttcccc agatcagcaa cgccactgac 350  
cgcaagtacc tggtcattgg tgacctgctc ttctcagctc tctggacctt 400

cctgtggttt gttggtttct gcttcctcac caaccagtgg gcagtcacca 450  
 acccgaagga cgtgctggtg ggggccgact ctgtgagggc agccatcacc 500  
 ttcagcttct tttccatctt ctctggggt gtgctggcct ccctggccta 550  
 ccagcgctac aaggctggcg tggacgactt catccagaat tacgttgacc 600  
 ccaactccga cccaacact gcctacgcct cctaccagg tgcatctgtg 650  
 gacaactacc aacagccacc cttcaccag aacgcggaga ccaccgaggg 700  
 ctaccagccg cccctgtgt actgagtggc ggttagcgtg ggaaggggga 750  
 cagagagggc cctccctct gccctggact ttcccatcag cctcctggaa 800  
 ctgccagccc ctctctttca cctgttccat cctgtgcagc tgacacacag 850  
 ctaaggagcc tcatagcctg gcgggggctg gcagagccac accccaagt 900  
 cctgtgcca gagggcttca gtcagccgt cactcctcca gggcactttt 950  
 aggaaaggg ttttagctag tgtttttct cgcttttaac gacctcagcc 1000  
 ccgcctgcag tggctagaag ccagcaggtg cccatgtgct actgacaagt 1050  
 gcctcagctt cccccggcc cgggtcaggc cgtgggagcc gctattatct 1100  
 gcgttctctg ccaaagactc gtgggggcca tcacacctgc cctgtgcagc 1150  
 ggagccggac caggctcttg tgcctcact caggtttgct tccctgtgc 1200  
 ccaactgctgt atgatctggg ggccaccacc ctgtgccgtt ggctctggg 1250  
 ctgcctcccg tgggtgagg gcggggctgg tgctcatggc acttctctct 1300  
 tgctcccacc cctggcagca gggaagggt ttgcctgaca acaccagct 1350  
 ttatgtaa atctctgagt tgttacttag gaagcctggg gagggcaggg 1400  
 gtgccccatg gctcccagac tctgtctgtg ccgagtgtat tataaatcgc 1450  
 tgggggagat gcccgccctg ggatgctgtt tggagacgga ataatgttt 1500  
 tctcattcaa ag 1512

<210> 162  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<400> 162  
 Met Glu Ser Gly Ala Tyr Gly Ala Ala Lys Ala Gly Gly Ser Phe  
 1 5 10 15  
 Asp Leu Arg Arg Phe Leu Thr Gln Pro Gln Val Val Ala Arg Ala  
 20 25 30

Val Cys Leu Val Phe Ala Leu Ile Val Phe Ser Cys Ile Tyr Gly  
 35 40 45  
 Glu Gly Tyr Ser Asn Ala His Glu Ser Lys Gln Met Tyr Cys Val  
 50 55 60  
 Phe Asn Arg Asn Glu Asp Ala Cys Arg Tyr Gly Ser Ala Ile Gly  
 65 70 75  
 Val Leu Ala Phe Leu Ala Ser Ala Phe Phe Leu Val Val Asp Ala  
 80 85 90  
 Tyr Phe Pro Gln Ile Ser Asn Ala Thr Asp Arg Lys Tyr Leu Val  
 95 100 105  
 Ile Gly Asp Leu Leu Phe Ser Ala Leu Trp Thr Phe Leu Trp Phe  
 110 115 120  
 Val Gly Phe Cys Phe Leu Thr Asn Gln Trp Ala Val Thr Asn Pro  
 125 130 135  
 Lys Asp Val Leu Val Gly Ala Asp Ser Val Arg Ala Ala Ile Thr  
 140 145 150  
 Phe Ser Phe Phe Ser Ile Phe Ser Trp Gly Val Leu Ala Ser Leu  
 155 160 165  
 Ala Tyr Gln Arg Tyr Lys Ala Gly Val Asp Asp Phe Ile Gln Asn  
 170 175 180  
 Tyr Val Asp Pro Thr Pro Asp Pro Asn Thr Ala Tyr Ala Ser Tyr  
 185 190 195  
 Pro Gly Ala Ser Val Asp Asn Tyr Gln Gln Pro Pro Phe Thr Gln  
 200 205 210  
 Asn Ala Glu Thr Thr Glu Gly Tyr Gln Pro Pro Pro Val Tyr  
 215 220

<210> 163  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 163  
 tggctcttcgc cttgatcgtg ttct 24

<210> 164  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 164  
gtgtactgag cggcggtag 20

<210> 165  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 165  
ctgaaggtag tggctgccct cac 23

<210> 166  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 166  
ccaggaggct catgggaaag tcc 23

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 167  
ccacgagtct aagcagatgt actgcgtggt caaccgcaac gaggatgcct 50

<210> 168  
<211> 3143  
<212> DNA  
<213> Homo sapiens

<400> 168  
gagccaccta cctgctccg aggccaggcc tgcagggcct catcgccag 50  
agggtgatca gtgagcagaa ggatgccgt ggccgaggcc cccaggtgg 100  
ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150  
atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200  
cctggtgccc ctgtttgtgc tgctggccct gctcgtgctg gcttcggcgg 250  
gggtgctact ctggtatttc ctagggtaca aggcggaggt gatggtcagc 300  
caggtgtact caggcagtct gcgtgtactc aatcgccact tctcccagga 350  
tcttaccgcg cggaatcta gtgccttccg cagtgaacc gccaaagccc 400

agaagatgct caaggagctc atcaccagca cccgcctggg aacttactac 450  
 aactccagct ccgtctattc ctttggggag ggacccctca cctgcttctt 500  
 ctggttcatt ctccaaatcc ccgagcaccg ccggtgatg ctgagccccg 550  
 aggtggtgca ggcactgctg gtggaggagc tgctgtccac agtcaacagc 600  
 tcggctgccg tcccctacag ggccgagtac gaagtggacc ccgagggcct 650  
 agtgcctctg gaagccagtg tgaaagacat agctgcattg aattccacgc 700  
 tgggttgta ccgtacagc tacgtgggcc agggccaggt cctccggctg 750  
 aaggggcctg accacctggc ctccagctgc ctgtggcacc tgcagggccc 800  
 caaggacctc atgtctaaac tccggctgga gtggacgctg gcagagtgcc 850  
 gggaccgact ggccatgtat gacgtggccg gggccctgga gaagaggctc 900  
 atcacctcgg tgtacggctg cagccgccag gagcccgtgg tggaggttct 950  
 ggcgtcgggg gccatcatgg cggctgtctg gaagaagggc ctgcacagct 1000  
 actacgaccc ctctgtgctc tccgtgcagc cgggtgtctt ccaggcctgt 1050  
 gaagtgaacc tgacgtgga caacaggctc gactcccagg gcgtcctcag 1100  
 caccctgtac ttccccagct actactgcc ccaaaccac tgctcctggc 1150  
 acctcacggt gccctctctg gactacggt tggccctctg gtttgatgcc 1200  
 tatgcactga ggaggcagaa gtatgattg ccgtgcaccc agggccagt 1250  
 gacgatccag aacaggaggc tgtgtggctt gcgcctctg cagccctacg 1300  
 ccgagaggat ccccggtgtg gccacggccg ggatcaccat caacttcacc 1350  
 tccagatct ccctaccgg gcccggtgtg cgggtgcact atggcttgta 1400  
 caaccagtgc gaccctgcc ctggagagtt cctctgttct gtgaatggac 1450  
 tctgtgtccc tgctgtgat ggggtcaagg actgcccac cggcctggat 1500  
 gagagaaact gcgtttgcag agccacattc cagtgcacaa aggacagcac 1550  
 atgcatctca ctgcccagg tctgtgatgg gcagcctgat tgtctcaacg 1600  
 gcagcgatga agagcagtgc caggaagggg tgccatgtgg gacattcacc 1650  
 ttccagtgtg aggaccggag ctgctgaag aagcccaacc cgcagtgtga 1700  
 tgggcggccc gactgcagg acggctcgga tgaggagcac tgtgactgtg 1750  
 gcctccaggg cccctccagc cgcattgttg gtggagctgt gtcctccag 1800  
 ggtgagtggc catggcaggc cagcctccag gttcggggtc gacacatctg 1850



total: 4302 bp

tgggggggcc ctcatcgctg accgctgggt gataacagct gccactgct 1900  
tccaggagga cagcatggcc tccacgggtc tgtggaccgt gttcctgggc 1950  
aagggtgggc agaactcgcg ctggcctgga gaggtgtcct tcaaggtgag 2000  
ccgcctgctc ctgcacccgt accacgaaga ggacagccat gactacgacg 2050  
tggcgctgct gcagctcgac caccgggtgg tgcgctcggc cgccgtgcgc 2100  
cccgtctgcc tgcccgcgcg ctcccacttc ttcgagccg gcctgcactg 2150  
ctggattacg ggctggggcg ccttgcgcg gggcgggccc atcagcaacg 2200  
ctctgcagaa agtggatgtg cagttgatcc cacaggacct gtgcagcgag 2250  
gcctatcgct accaggtgac gccacgcatg ctgtgtgccg gctaccgcaa 2300  
gggcaagaag gatgcctgtc aggggtgactc aggtggtccg ctggtgtgca 2350  
aggcactcag tggccgctgg ttctggcgcg ggctggtcag ctggggcctg 2400  
ggctgtggcc ggcctaacta cttcggcgtc tacacccgca tcacaggtgt 2450  
gatcagctgg atccagcaag tggtagcctg aggaactgcc cccctgcaaa 2500  
gcagggccca cctcctggac tcagagagcc cagggcaact gccaagcagg 2550  
gggacaagta ttctggcggg ggggtgggga gagagcaggc cctgtggtgg 2600  
caggaggtgg catcttgtct cgtccctgat gtctgtcca gtgatggcag 2650  
gaggatggag aagtgccagc agctgggggt caagacgtcc cctgaggacc 2700  
caggcccaca ccagccctt ctgcctccca attctctctc ctccgtcccc 2750  
ttctccact gctgcctaata gcaaggcagt ggctcagcag caagaatgct 2800  
ggttctacat cccgaggagt gtctgaggtg cgcccactc tgtacagagg 2850  
ctgtttgggc agccttgctt ccagagagca gattccagct tcggaagccc 2900  
ctggtctaac ttgggatctg ggaatggaag gtgctcccat cggaggggac 2950  
cctcagagcc ctggagactg ccagggtggc ctgctgccac tgtaagccaa 3000  
aagggtggga agtcttgact ccagggtcct tgcccacccc ctgcctgcca 3050  
cctgggccct cacagcccag accctcactg ggaggtgagc tcagctgccc 3100  
tttgaataa agctgcctga tcaaaaaaaaa aaaaaaaaaa aaa 3143

<210> 169  
<211> 802  
<212> PRT  
<213> Homo sapiens  
  
<400> 169

TECHNICAL REPORT

Met	Pro	Val	Ala	Glu	Ala	Pro	Gln	Val	Ala	Gly	Gly	Gln	Gly	Asp	1	5	10	15
Gly	Gly	Asp	Gly	Glu	Glu	Ala	Glu	Pro	Glu	Gly	Met	Phe	Lys	Ala	20	25	30	
Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	35	40	45	
Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly	50	55	60	
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val	65	70	75	
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe	80	85	90	
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu	95	100	105	
Thr	Ala	Lys	Ala	Gln	Lys	Met	Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr	110	115	120	
Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly	125	130	135	
Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro	140	145	150	
Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu	155	160	165	
Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val	170	175	180	
Pro	Tyr	Arg	Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly	Leu	Val	Ile	185	190	195	
Leu	Glu	Ala	Ser	Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser	Thr	Leu	200	205	210	
Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg	215	220	225	
Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu	230	235	240	
Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr	245	250	255	
Leu	Ala	Glu	Cys	Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly	260	265	270	
Pro	Leu	Glu	Lys	Arg	Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg	275	280	285	
Gln	Glu	Pro	Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala				

	290		295		300
Val. Val Trp Lys	Lys Gly Leu His Ser	Tyr Tyr Asp Pro Phe	Val		
	305		310		315
Leu Ser Val Gln	Pro Val Val Phe Gln	Ala Cys Glu Val Asn	Leu		
	320		325		330
Thr Leu Asp Asn	Arg Leu Asp Ser Gln	Gly Val Leu Ser Thr	Pro		
	335		340		345
Tyr Phe Pro Ser	Tyr Tyr Ser Pro Gln	Thr His Cys Ser Trp	His		
	350		355		360
Leu Thr Val Pro	Ser Leu Asp Tyr Gly	Leu Ala Leu Trp Phe	Asp		
	365		370		375
Ala Tyr Ala Leu	Arg Arg Gln Lys Tyr	Asp Leu Pro Cys Thr	Gln		
	380		385		390
Gly Gln Trp Thr	Ile Gln Asn Arg Arg	Leu Cys Gly Leu Arg	Ile		
	395		400		405
Leu Gln Pro Tyr	Ala Glu Arg Ile Pro	Val Val Ala Thr Ala	Gly		
	410		415		420
Ile Thr Ile Asn	Phe Thr Ser Gln Ile	Ser Leu Thr Gly Pro	Gly		
	425		430		435
Val Arg Val His	Tyr Gly Leu Tyr Asn	Gln Ser Asp Pro Cys	Pro		
	440		445		450
Gly Glu Phe Leu	Cys Ser Val Asn Gly	Leu Cys Val Pro Ala	Cys		
	455		460		465
Asp Gly Val Lys	Asp Cys Pro Asn Gly	Leu Asp Glu Arg Asn	Cys		
	470		475		480
Val Cys Arg Ala	Thr Phe Gln Cys Lys	Glu Asp Ser Thr Cys	Ile		
	485		490		495
Ser Leu Pro Lys	Val Cys Asp Gly Gln	Pro Asp Cys Leu Asn	Gly		
	500		505		510
Ser Asp Glu Glu	Gln Cys Gln Glu Gly	Val Pro Cys Gly Thr	Phe		
	515		520		525
Thr Phe Gln Cys	Glu Asp Arg Ser Cys	Val Lys Lys Pro Asn	Pro		
	530		535		540
Gln Cys Asp Gly	Arg Pro Asp Cys Arg	Asp Gly Ser Asp Glu	Glu		
	545		550		555
His Cys Asp Cys	Gly Leu Gln Gly Pro	Ser Ser Arg Ile Val	Gly		
	560		565		570
Gly Ala Val Ser	Ser Glu Gly Glu Trp	Pro Trp Gln Ala Ser	Leu		
	575		580		585

Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala Asp  
590 595 600

Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met  
605 610 615

Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln  
620 625 630

Asn Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu  
635 640 645

Leu Leu His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val  
650 655 660

Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val  
665 670 675

Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly  
680 685 690

Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly  
695 700 705

Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro  
710 715 720

Gln Asp Leu Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg  
725 730 735

Met Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln  
740 745 750

Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg  
755 760 765

Trp Phe Leu Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg  
770 775 780

Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser  
785 790 795

Trp Ile Gln Gln Val Val Thr  
800

<210> 170  
<211> 1327  
<212> DNA  
<213> Homo sapiens

<400> 170  
gcacccaggg ccagtggacg atccagaaca ggaggctgtg tggttgccg 50  
atcctgcagc cctacgccga gaggatcccc gtggtggcca cggccgggat 100  
caccatcaac ttcacctccc agatctccct caccggggccc ggtgtgcggg 150  
tgcaactatgg cttgtacaac cagtgggacc cctgccctgg agagttcctc 200

tgttctgtga atggactctg tgtccctgcc tgtgatgggg tcaaggactg 250  
 ccccaacggc ctggatgaga gaaactgctg ttgcagagcc acattccagt 300  
 gcaaagagga cagcacatgc atctcactgc ccaaggtctg tgatgggcag 350  
 cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400  
 atgtgggaca ttacacttcc agtgtgagga ccggagctgc gtgaagaagc 450  
 ccaacccgca gtgtgatggg cggcccgcact gcagggacgg ctccgatgag 500  
 gagcaactgtg actgtggcct ccagggcccc tccagccgca ttgttggtgg 550  
 agctgtgtcc tccgaggggt agtggccatg gcaggccagc ctccaggttc 600  
 ggggtcgaca catctgtggg gggggccctca tcgctgaccg ctgggtgata 650  
 acagctgccc actgcttcca ggaggacagc atggcctcca cgggtgctgtg 700  
 gaccgtgttc ctgggcaagg tgtggcagaa ctgcgcctgg cctggagagg 750  
 tgtccttcaa ggtgagccgc ctgctcctgc acccgtaacca cgaagaggac 800  
 agccatgact acgacgtggc gctgctgcag ctgcaccacc cgggtggtgcg 850  
 ctgcgccgcc gtgcgccccg tctgcctgcc cgcgcgctcc cacttcttcg 900  
 agccccgcct gcaactgctg attacgggtt ggggcgcctt gcgcgagggc 950  
 ggccccatca gcaacgctct gcagaaagtg gatgtgcagt tgatcccaca 1000  
 ggacctgtgc agcgaggcct atcgctacca ggtgacgcca cgcattgctgt 1050  
 gtgccggcta ccgcaagggc aagaaggatg cctgtcaggg tgactcaggt 1100  
 ggtccgctgg tgtgcaaggc actcagtggc cgctggttcc tggcggggct 1150  
 ggtcagctgg ggccctgggt gtggccggcc taactacttc ggcgctctaca 1200  
 cccgcattcac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250  
 actgcccccc tgcaaagcag ggcccacctc ctggactcag agagcccagg 1300  
 gcaactgcca agcaggggga caagtat 1327

<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc ccaactgcttc cagg 24

<210> 172

<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 172  
taatccagca gtgcaggccg gg 22

<210> 173  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 173  
atggcctcca cgtgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 174  
tgcctatgca ctgaggaggc agaag 25

<210> 175  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 175  
aggcaggac acagagtcca ttcac 25

<210> 176  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 176  
agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177  
<211> 1510  
<212> DNA  
<213> Homo sapiens

<400> 177

ggacgagggc agatctcggt ctggggcaag ccgttgacac tcgctccctg 50  
ccaccgcccg ggctccgtgc cgccaagttt tcattttcca ctttctctgc 100  
ctccagtccc ccagcccctg gccgagagaa ggggtcttacc ggccgggatt 150  
gctggaaaca ccaagaggtg gtttttggtt tttaaaactt ctgtttcttg 200  
ggaggggggtg tggcggggca ggatgagcaa ctccgttcct ctgctctgtt 250  
tctggagcct ctgctattgc tttgctgcgg ggagcccctg accttttggt 300  
ccagagggac ggctggaaga taagctccac aaacccaaag ctacacagac 350  
tgaggtcaaa ccattctgtg ggtttaacct ccgcacctcc aaggaccag 400  
agcatgaagg atgctacctc tccgtcggcc acagccagcc cttagaagac 450  
tgcagtttca acatgacagc taaaacctt ttcatcattc acggatggac 500  
gatgagcggg atctttgaaa actggctgca caaactcgtg tcagccctgc 550  
acacaagaga gaaagacgcc aatgtagttg tgggtgactg gctccccctg 600  
gcccaccagc ttacacgga tgcggtcaat aataccaggg tgggtgggaca 650  
cagcattgcc aggatgctcg actggctgca ggagaaggac gatttttctc 700  
tcgggaatgt ccacttgatc ggctacagcc tcggagcgca cgtggccggg 750  
tatgcaggca acttcgtgaa aggaacgggt ggccgaatca caggtttgga 800  
tcctgccggg cccatgtttg aaggggccga catccacaag aggtctctc 850  
cggacgatgc agatttttg gatgtcctcc acacctacac gcgttcctc 900  
ggcttgagca ttggtattca gatgcctgtg ggccacattg acatctacc 950  
caatgggggt gacttccagc caggctgtgg actcaacgat gtcttgggat 1000  
caattgcata tggaacaatc acagaggtg taaaatgtga gcatgagcg 1050  
gccgtccacc tctttgttga ctctctggtg aatcaggaca agccgagttt 1100  
tgccctccag tgactgact ccaatcgctt caaaaagggg atctgtctga 1150  
gctgccgcaa gaaccgttgt aatagcattg gctacaatgc caagaaaatg 1200  
aggaacaaga ggaacagcaa aatgtaccta aaaacccggg caggcatgcc 1250  
tttcagaggt aaccttcagt ccctggagtg tccctgagga aggcccttaa 1300  
tacctccttc ttaataccat gctgcagagc agggcacatc ctgcccagg 1350  
agaagtggcc agcacaatcc aatcaaatcg ttgcaaatca gattacactg 1400  
tgcatgtcct aggaagggga atctttacaa aataaacagt gtggaccct 1450

aataaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaaaa 1510

<210> 178

<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr  
1 5 10 15

Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg  
20 25 30

Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val  
35 40 45

Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu  
50 55 60

His Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu  
65 70 75

Asp Cys Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His  
80 85 90

Gly Trp Thr Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu  
95 100 105

Val Ser Ala Leu His Thr Arg Glu Lys Asp Ala Asn Val Val Val  
110 115 120

Val Asp Trp Leu Pro Leu Ala His Gln Leu Tyr Thr Asp Ala Val  
125 130 135

Asn Asn Thr Arg Val Val Gly His Ser Ile Ala Arg Met Leu Asp  
140 145 150

Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu Gly Asn Val His Leu  
155 160 165

Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly Tyr Ala Gly Asn  
170 175 180

Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu Asp Pro Ala  
185 190 195

Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu Ser Pro  
200 205 210

Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg Ser  
215 220 225

Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp  
230 235 240

Footnote: The Foot



Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn	
245	250 255
Asp Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val	
260	265 270
Lys Cys Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu	
275	280 285
Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser	
290	295 300
Asn Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg	
305	310 315
Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg	
320	325 330
Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg	
335	340 345
Gly Asn Leu Gln Ser Leu Glu Cys Pro	
350	

TOUCHSTONE

<210> 179  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 179  
 gtgagcatga gcgagccgtc cac 23

<210> 180  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 180  
 gctattacaa cggttcttgc ggcagc 26

<210> 181  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 181  
 ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240  
<212> DNA  
<213> Homo sapiens

<400> 182  
cggacgcgtg ggaggacgcg tgggcctggg caagggccgg ggcgcggggc 50  
cgagccacct cttccctccc cccgcttccc tgtcgcgctc cgctggctgg 100  
acgcgctgga ggagtggagc agcaccgggc cgccctggg ggctgacagt 150  
cggcaaagtt tggcccgaag aggaagtggc ctcaaaccgc ggaggtggc 200  
gaccaggcca gaccaggggc gctcgtgcc tgcgggcggg ctgtaggcga 250  
gggcgcgccc cagtgcgag acccggggct tcaggagccg gccccgggag 300  
agaagagtgc ggaggcggac ggagaaaaca actccaaagt tggcgaaagg 350  
caccgcccct actccgggc tgcgcgcgc tccccgccc cagccctggc 400  
atccagagta cgggtcgagc ccgggccatg gagccccct ggggaggcgg 450  
caccagggag cctgggcgcc cggggctccg ccgcgacccc atcgggtaga 500  
ccacagaagc tccgggaccc ttccggcacc tctggacagc ccaggatgct 550  
gttgccacc ctctctctcc tctctcttg aggcgtctg gcccatccag 600  
accgattat ttttccaaat catgcttggt agggcccccc agcagtgtc 650  
ttagaagtgc agggcacctt acagaggccc ctggtccggg acagccgcac 700  
ctcccctgcc aactgcacct ggctcactc gggcagcaag gaacagactg 750  
tcaccatcag gtccagaag ctacacctgg cctgtggctc agagcgctta 800  
accctaogct cccctctcca gccactgatc tccctgtgtg aggcacctcc 850  
cagccctctg cagctgcccg ggggcaacgt caccatcact tacagctatg 900  
ctggggccag agcaccatg ggccagggct tctgtctctc ctacagccaa 950  
gattggctga tgtgcctgca ggaagagttt cagtgcctga accaccgctg 1000  
tgtatctgct gtccagcgt gtgatggggg tgatgcctgt ggcgatggct 1050  
ctgatgaagc aggttgacgc tcagaccct tccctggcct gacccaaga 1100  
cccgctccct cctgccttg caatgtcacc ttggaggact tctatgggg 1150  
cttctctct cctggatata cacacctagc ctcatctcc caccctcagt 1200  
cctgccattg gctgctggac ccccatgatg gccggcggct ggccgtgcgc 1250  
ttcacagccc tggacttggg ctttgagat gcagtgcagc tgtatgacgg 1300  
ccctgggccc cctgagagct cccgactact gcgtagtctc acccattca 1350

gcaatggcaa ggctgtcaact gtggagacac tgtctggcca ggctgttg 1400  
 tcctaccaca cagttgcttg gagcaatggt cgtggcttca atgccaccta 1450  
 ccatgtgcgg ggctattgct tgccttggga cagacctgt ggcttaggct 1500  
 ctggcctggg agctggcgaa ggcctagggt agcgtgcta cagtgaggca 1550  
 cagcgtgtg acggctcatg ggactgtgct gacggcacag atgaggagga 1600  
 ctgcccaggc tgcccacctg gacacttccc ctgtggggct gctggcacct 1650  
 ctggtgccac agcctgctac ctgctgctg accgtgcaa ctaccagact 1700  
 ttctgtgctg atggagcaga tgagagacgc tgtcggcatt gccagcctgg 1750  
 caatttccga tgccgggacg agaagtgcgt gtatgagacg tgggtgtgcg 1800  
 atgggcagcc agactgtgcg gacggcagtg atgagtggga ctgctcctat 1850  
 gttctgcccc gcaaggtoat tacagctgca gtcattggca gcctagtgtg 1900  
 cggcctgtc ctggtcatcg ccctgggctg cacctgcaag ctctatgcc 1950  
 ttgcaccca ggagtacagc atctttgccc ccctctccc gatggaggct 2000  
 gagattgtgc agcagcaggc accccttcc tacgggcagc tcattgccc 2050  
 gggtgccatc ccacctgtag aagacttcc tacagagaat cctaataata 2100  
 actcagtgtc gggcaacctg cgttctctgc tacagatctt acgccaggat 2150  
 atgactccag gaggtggccc aggtgcccgc cgtcgtcagc ggggccgctt 2200  
 gatgcgacgc ctggtacgcc gtctccgccc ctggggcttg ctccctcgaa 2250  
 ccaacacccc ggctcgggcc tctgaggcca gatcccaggc cacaccttct 2300  
 gctgctcccc ttgaggccct agatggtggc acaggccagc cccgtgaggg 2350  
 cggggcagtg ggtgggcaag atggggagca ggcaccccca ctgcccata 2400  
 aggctccct cccatctgct agcacgtctc cagccccac tactgtccct 2450  
 gaagccccag ggccactgcc ctactgccc ctagagccat cactattgtc 2500  
 tggagtgtg caggccctgc gaggcgcct gttgccagc ctggggcccc 2550  
 caggaccaac ccggagcccc cctggacccc acacagcagt cctggccctg 2600  
 gaagatgagg acgatgtgct actggtgcca ctggtgagc cgggggtgtg 2650  
 ggtagctgag gcagaggatg agccactgct tacctgaggg gacctggggg 2700  
 ctctactgag gcctctcccc tgggggtct actcatagtg gcacaacctt 2750  
 ttagaggtgg gtcagcctcc cctccaccac ttccttccct gtcctggat 2800

ttcagggact tggtaggcct cccgttgacc ctatgtagct gctataaagt 2850  
 taagtgtccc tcaggcaggg agagggctca cagagtctcc tctgtacgtg 2900  
 gccatggcca gacacccag tcccttcacc accacctgct cccacgcca 2950  
 ccaccatttg ggtggctggt tttaaaaagt aaagttctta gaggatcata 3000  
 ggtctggaca ctccatcctt gccaaacctc tacccaaaag tggccttaag 3050  
 caccggaatg ccaattaact agagaccctc cagcccccaa ggggaggatt 3100  
 tgggcagaac ctgaggtttt gccatccaca atccctccta cagggcctgg 3150  
 ctacacaaaa gagtgcaaca aatgcttcta ttccatagct acggcattgc 3200  
 tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183  
 <211> 713  
 <212> PRT  
 <213> Homo sapiens

T  
O  
P  
S  
E  
Q  
U  
E  
N  
C  
E

<400> 183  
 Met Leu Leu Ala Thr Leu Leu Leu Leu Leu Gly Gly Ala Leu  
 1 5 10 15  
 Ala His Pro Asp Arg Ile Ile Phe Pro Asn His Ala Cys Glu Asp  
 20 25 30  
 Pro Pro Ala Val Leu Leu Glu Val Gln Gly Thr Leu Gln Arg Pro  
 35 40 45  
 Leu Val Arg Asp Ser Arg Thr Ser Pro Ala Asn Cys Thr Trp Leu  
 50 55 60  
 Ile Leu Gly Ser Lys Glu Gln Thr Val Thr Ile Arg Phe Gln Lys  
 65 70 75  
 Leu His Leu Ala Cys Gly Ser Glu Arg Leu Thr Leu Arg Ser Pro  
 80 85 90  
 Leu Gln Pro Leu Ile Ser Leu Cys Glu Ala Pro Pro Ser Pro Leu  
 95 100 105  
 Gln Leu Pro Gly Gly Asn Val Thr Ile Thr Tyr Ser Tyr Ala Gly  
 110 115 120  
 Ala Arg Ala Pro Met Gly Gln Gly Phe Leu Leu Ser Tyr Ser Gln  
 125 130 135  
 Asp Trp Leu Met Cys Leu Gln Glu Glu Phe Gln Cys Leu Asn His  
 140 145 150  
 Arg Cys Val Ser Ala Val Gln Arg Cys Asp Gly Val Asp Ala Cys  
 155 160 165  
 Gly Asp Gly Ser Asp Glu Ala Gly Cys Ser Ser Asp Pro Phe Pro



Leu Tyr Ala Ile	Arg Thr Gln Glu Tyr	Ser Ile Phe Ala Pro	Leu
	470	475	480
Ser Arg Met Glu	Ala Glu Ile Val Gln	Gln Gln Ala Pro Pro	Ser
	485	490	495
Tyr Gly Gln Leu	Ile Ala Gln Gly Ala	Ile Pro Pro Val Glu	Asp
	500	505	510
Phe Pro Thr Glu	Asn Pro Asn Asp Asn	Ser Val Leu Gly Asn	Leu
	515	520	525
Arg Ser Leu Leu	Gln Ile Leu Arg Gln	Asp Met Thr Pro Gly	Gly
	530	535	540
Gly Pro Gly Ala	Arg Arg Arg Gln Arg	Gly Arg Leu Met Arg	Arg
	545	550	555
Leu Val Arg Arg	Leu Arg Arg Trp Gly	Leu Leu Pro Arg Thr	Asn
	560	565	570
Thr Pro Ala Arg	Ala Ser Glu Ala Arg	Ser Gln Val Thr Pro	Ser
	575	580	585
Ala Ala Pro Leu	Glu Ala Leu Asp Gly	Gly Thr Gly Pro Ala	Arg
	590	595	600
Glu Gly Gly Ala	Val Gly Gly Gln Asp	Gly Glu Gln Ala Pro	Pro
	605	610	615
Leu Pro Ile Lys	Ala Pro Leu Pro Ser	Ala Ser Thr Ser Pro	Ala
	620	625	630
Pro Thr Thr Val	Pro Glu Ala Pro Gly	Pro Leu Pro Ser Leu	Pro
	635	640	645
Leu Glu Pro Ser	Leu Leu Ser Gly Val	Val Gln Ala Leu Arg	Gly
	650	655	660
Arg Leu Leu Pro	Ser Leu Gly Pro Pro	Gly Pro Thr Arg Ser	Pro
	665	670	675
Pro Gly Pro His	Thr Ala Val Leu Ala	Leu Glu Asp Glu Asp	Asp
	680	685	690
Val Leu Leu Val	Pro Leu Ala Glu Pro	Gly Val Trp Val Ala	Glu
	695	700	705
Ala Glu Asp Glu	Pro Leu Leu Thr		
	710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184  
 ggctgtcact gtggagacac 20  
  
 <210> 185  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 185  
 gcaaggtcat tacagctg 18  
  
 <210> 186  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 186  
 agaacatagg agcagtccca ctc 23  
  
 <210> 187  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 187  
 tgcctgctgc tgcacaatct cag 23  
  
 <210> 188  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 188  
 ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45  
  
 <210> 189  
 <211> 663  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 189  
 cgagctgggc gagaagtagg ggagggcggg gctccgccgc ggtggcggtt 50  
  
 gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100  
  
 gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150



aataaaacat cgccccttct gcttcagtgt gaaaggccac gtgaagatgc 200  
tgcggtggc actaactgtg acatctatga ccttttttat catcgacaaa 250  
gccccgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300  
atttttcata cttttatatg tactcagact tgatcgatta atgaagtggt 350  
tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400  
atgctcatcg tatctgtgtt ggactgata ccagaaacca caacattgac 450  
agttggtgga ggggtgtttg cacttgtagc agcagtatgc tgtcttgccg 500  
acggggccct tattaccgg aagcttctgt tcaatcccag cggtccttac 550  
cagaaaaagc ctgtgcatga aaaaaaagaa gttttgtaat tttatattac 600  
tttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650  
aaaaaaaaa aaa 663

<210> 190  
<211> 152  
<212> PRT  
<213> Homo sapiens

<400> 190  
Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe  
1 5 10 15  
Ser Val Lys Gly His Val Lys Met Leu Arg Leu Ala Leu Thr Val  
20 25 30  
Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr  
35 40 45  
Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile  
50 55 60  
Leu Leu Tyr Val Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe  
65 70 75  
Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe  
80 85 90  
Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr  
95 100 105  
Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys  
110 115 120  
Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn  
125 130 135  
Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu  
140 145 150





Val Leu

<210> 191  
<211> 495  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 78, 212, 234, 487  
<223> unknown base

<400> 191  
gggcgagaag taggggaggg cgtgttcgc gcggtggcg gttgctatcg 50  
ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100  
ctgctgctgg gtctgcagac gcatggata acgtgcagcc gaaaataaaa 150  
catcgccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200  
ggcactaact gngacatcta tgacctttt tatnatcgca caagcccctg 250  
aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300  
atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350  
gcctttgctt gatattatca actcactggt aacaacagta ttcatgctca 400  
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450  
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 192  
cgttttgcag aacctactca ggcag 25

<210> 193  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 193  
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194  
<211> 40

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 194  
aaagtgtctgc tgcctgggtct gcagacgcga tggataacgt 40

<210> 195  
<211> 1879  
<212> DNA  
<213> Homo sapien

<400> 195  
cagccccgcg cgccggccga gtcgtgagc cgcggctgcc ggacgggacg 50  
ggacgggcta ggctgggccc gccccccggg ccccgccgtg ggcatgggcg 100  
cactggcccc ggctgtctgc ctgcctctgc tggcccagtg gctcctgcgc 150  
gccgcccccg agctggcccc cgcgcccttc acgtgcccc tccgggtggc 200  
cgcggccacg aaccgcgtag ttgcgccac cccgggaccc gggacccttg 250  
ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgcctggcg 300  
tccccgcgg gcgcgcgcaa cttcttgcc atggtagaca acctgcaggg 350  
ggactctggc cgcggctact acctggagat gctgatcggg accccccgc 400  
agaagctaca gattctcgtt gacactggaa gcagtaactt tgccgtggca 450  
ggaacccccg actctacat agacacgtac ttgacacag agaggtctag 500  
cacataccgc tccaagggct ttgacgtcac agtgaagtac acacaaggaa 550  
gctggacggg cttcgttggg gaagacctcg tcaccatccc caaaggcttc 600  
aatacttctt ttcttgtaa cattgccact atttttgaat cagagaattt 650  
ctttttgcct gggattaaat ggaatggaat acttggccta gcttatgcca 700  
cacttgccaa gccatcaagt tctctggaga ccttcttoga ctccctggtg 750  
acacaagcaa acatcccaa cgttttctcc atgcagatgt gtggagccgg 800  
cttgcccgtt gctggatctg ggaccaacgg aggtagtctt gtcttgggtg 850  
gaattgaacc aagtttgtat aaaggagaca tctggtatac ccctattaag 900  
gaagagtggc actaccagat agaaattctg aaattggaaa ttggaggcca 950  
aagccttaat ctggactgca gagagtataa cgagacaag gccatcgtgg 1000  
acagtggcac cagctgctg cgctgcccc agaaggtgtt tgatgcgggtg 1050  
gtggaagctg tggccgcgc atctctgatt ccagaattct ctgatggttt 1100

ctggactggg tcccagctgg cgtgctggac gaattcggaa acaccttggt 1150  
 cttacttccc taaaatctcc atctacctga gagacgagaa ctccagcagg 1200  
 tcattccgta tcacaatcct gcctcagctt tacattcagc ccatgatggg 1250  
 ggccggcctg aattatgaat gttaccgatt cggcatttcc ccatccacaa 1300  
 atgcgctggg gatcggtgcc acggtgatgg agggcttcta cgtcatcttc 1350  
 gacagagccc agaagagggt gggcttcgca gcgagcccct gtgcagaaat 1400  
 tgcagggtgct gcagtgtctg aaatttccgg gcctttctca acagaggatg 1450  
 tagccagcaa ctgtgtcccc gctcagtctt tgagcgagcc cattttgtgg 1500  
 attgtgtcct atgcgtcat gagcgtctgt ggagccatcc tccttgtctt 1550  
 aatcgtcctg ctgctgctgc cgttcgggtg tcagcgtcgc ccccgtagcc 1600  
 ctgaggctcg caatgatgag tcctctctgg tcagacatcg ctggaaatga 1650  
 atagccaggc ctgacctcaa gcaaccatga actcagctat taagaaaatc 1700  
 acatttccag ggcagcagcc gggatcgatg gtggcgcttt ctctgtgcc 1750  
 caccgctctt caatctctgt tctgctccca gatgccttct agattcactg 1800  
 tcttttgatt ctgattttc aagctttcaa atcctcccta cttccaagaa 1850  
 aaataattaa aaaaaaaact tcattctaa 1879

<210> 196  
 <211> 518  
 <212> PRT  
 <213> Homo sapien

<400> 196  
 Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln  
 1 5 10 15  
 Trp Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr  
 20 25 30  
 Leu Pro Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro  
 35 40 45  
 Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu  
 50 55 60  
 Ala Leu Ala Leu Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala  
 65 70 75  
 Asn Phe Leu Ala Met Val Asp Asn Leu Gln Gly Asp Ser Gly Arg  
 80 85 90  
 Gly Tyr Tyr Leu Glu Met Leu Ile Gly Thr Pro Pro Gln Lys Leu  
 95 100 105

Gln Ile Leu Val	Asp Thr Gly Ser Ser	Asn Phe Ala Val Ala Gly	110	115	120
Thr Pro His Ser	Tyr Ile Asp Thr Tyr	Phe Asp Thr Glu Arg Ser	125	130	135
Ser Thr Tyr Arg	Ser Lys Gly Phe Asp	Val Thr Val Lys Tyr Thr	140	145	150
Gln Gly Ser Trp	Thr Gly Phe Val Gly	Glu Asp Leu Val Thr Ile	155	160	165
Pro Lys Gly Phe	Asn Thr Ser Phe Leu	Val Asn Ile Ala Thr Ile	170	175	180
Phe Glu Ser Glu	Asn Phe Phe Leu Pro	Gly Ile Lys Trp Asn Gly	185	190	195
Ile Leu Gly Leu	Ala Tyr Ala Thr Leu	Ala Lys Pro Ser Ser Ser	200	205	210
Leu Glu Thr Phe	Phe Asp Ser Leu Val	Thr Gln Ala Asn Ile Pro	215	220	225
Asn Val Phe Ser	Met Gln Met Cys Gly	Ala Gly Leu Pro Val Ala	230	235	240
Gly Ser Gly Thr	Asn Gly Gly Ser Leu	Val Leu Gly Gly Ile Glu	245	250	255
Pro Ser Leu Tyr	Lys Gly Asp Ile Trp	Tyr Thr Pro Ile Lys Glu	260	265	270
Glu Trp Tyr Tyr	Gln Ile Glu Ile Leu	Lys Leu Glu Ile Gly Gly	275	280	285
Gln Ser Leu Asn	Leu Asp Cys Arg Glu	Tyr Asn Ala Asp Lys Ala	290	295	300
Ile Val Asp Ser	Gly Thr Thr Leu Leu	Arg Leu Pro Gln Lys Val	305	310	315
Phe Asp Ala Val	Val Glu Ala Val Ala	Arg Ala Ser Leu Ile Pro	320	325	330
Glu Phe Ser Asp	Gly Phe Trp Thr Gly	Ser Gln Leu Ala Cys Trp	335	340	345
Thr Asn Ser Glu	Thr Pro Trp Ser Tyr	Phe Pro Lys Ile Ser Ile	350	355	360
Tyr Leu Arg Asp	Glu Asn Ser Ser Arg	Ser Phe Arg Ile Thr Ile	365	370	375
Leu Pro Gln Leu	Tyr Ile Gln Pro Met	Met Gly Ala Gly Leu Asn	380	385	390
Tyr Glu Cys Tyr	Arg Phe Gly Ile Ser	Pro Ser Thr Asn Ala Leu			

395	400	405
Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr Val Ile Phe Asp		
410	415	420
Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro Cys Ala Glu		
425	430	435
Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe Ser Thr		
440	445	450
Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser Glu		
455	460	465
Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly		
470	475	480
Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg		
485	490	495
Cys Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser		
500	505	510
Ser Leu Val Arg His Arg Trp Lys		
515		

<210> 197  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 197  
 cgagaagct acagattctc g 21

<210> 198  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 198  
 ggaaattgga ggccaaagc 19

<210> 199  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 199  
 ggatgtagcc agcaactgtg 20

<210> 200  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 200  
gccttgctc gttctcttc 19

<210> 201  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 201  
ggctctgtgc ctggatgg 18

<210> 202  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 202  
gacaagacta cctccgttgg tc 22

<210> 203  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 203  
tgatgcacag ttcagcacct gttg 24

<210> 204  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 204  
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205  
<211> 1939  
<212> DNA



<213> Homo sapiens

<400> 205

cgctccgcc ttccgaggt gacgcgccg ggcgccgttc caggcctgtg 50  
caggcgcat cggcagccgc ctggcgcca tccagggcgg tgcggggcct 100  
ggcgggagc cgggagggc ggccggcatg gaggcgtgc tgctgggcgc 150  
ggggttgctg ctgggcgtt acgtgcttgt ctactacaac ctggtgaagg 200  
ccccccgtg cggcgccatg ggcaacctgc ggggcgcac ggccgtggtc 250  
acgggcgcca acagcgcat cggaaagatg acggcgctgg agctggcgcg 300  
ccggggagcg cgcgtggtgc tggcctgcc cagccaggag cgcggggagg 350  
cggtgcctt cgacctccgc caggagagt ggaacaatga ggtcatcttc 400  
atggccttgg acttgccag tctggcctcg gtgcgggcct ttgccactgc 450  
ctttctgagc tctgagccac ggttgacat cctcatccac aatgcggta 500  
tcagttcctg tggccggacc cgtgaggcgt ttaacctgct gcttcgggtg 550  
aaccatatcg gtccctttct gctgacacat ctgctgctgc cttgcctgaa 600  
ggcatgtgcc cctagcccg tgggtggtgt agcctcagct gccactgtc 650  
ggggacgtct tgacttcaa cgcctggacc gccagtggt gggctggcgg 700  
caggagctgc gggcatatgc tgactaag ctggctaag tactgtttgc 750  
ccgggagctc gccaaccagc ttgaggccac tggcgtcacc tgctatgcag 800  
cccaccagg gcctgtgaac tcggagctgt tctgcgcca tgttcctgga 850  
tggctgcgcc cacttttgcg cccattggct tggctggtgc tccgggcacc 900  
aagagggggt gccagacac ccctgtattg tgctctacaa gagggcatcg 950  
agcccctcag tgggagatat ttgccaact gccatgtgga agaggtgcct 1000  
ccagctgccc gacagaccg ggcagccat cggtatggg aggcagcaa 1050  
gaggtggca gggcttggc ctggggagga tgctgaacc gatgaagacc 1100  
cccagtctga ggactcagag gcccctctt ctctaagcac cccccaccct 1150  
gaggagcca cagtttctca acctacccc agcctcaga gtcaccaga 1200  
tttgtctaag atgacgacc gaattcaggc taaagttgag cctgagatcc 1250  
agctctccta accctcaggc caggatgctt gccatggcac ttcattgtcc 1300  
ttgaaaacct cggatgtgtg tgaggccatg cctggacac tgacgggttt 1350  
gtgatcttga cctccgtggt tactttctgg ggcccaagc tgtgccctgg 1400

acatctcttt tcttggtga aggaataatg ggtgattatt tcttctgag 1450  
 agtgacagta accccagatg gagagatagg ggtatgctag acactgtgct 1500  
 tctcggaat ttggatgtag tattttcagg cccaccctt attgattctg 1550  
 atcagctctg gagcagaggc agggagtttg caatgtgatg cactgccaac 1600  
 attgagaatt agtgaactga tccctttgca accgtctagc taggtagtta 1650  
 aattaccccc atgttaatga agcggaatta ggctcccgag ctaagggact 1700  
 cgcctagggt ctcacagtga gtaggaggag ggctgggat ctgaacccaa 1750  
 gggctgagg ccagggccga ctgccgtaag atgggtgctg agaagtgagt 1800  
 cagggcaggg cagctggat cgaggtgcc catgggagta aggggacgcc 1850  
 ttccggcgg atgcagggt ggggtcatct gtatctgaag cccctcgaa 1900  
 taaagcgcgt tgaccgcaa aaaaaaaaa aaaaaaaaa 1939

<210> 206  
 <211> 377  
 <212> PRT  
 <213> Homo sapiens

<400> 206  
 Met Glu Ala Leu Leu Leu Gly Ala Gly Leu Leu Leu Gly Ala Tyr 15  
 1 5 10  
 Val Leu Val Tyr Tyr Asn Leu Val Lys Ala Pro Pro Cys Gly Gly 30  
 20 25  
 Met Gly Asn Leu Arg Gly Arg Thr Ala Val Val Thr Gly Ala Asn 45  
 35 40  
 Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly 60  
 50 55  
 Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala 75  
 65 70  
 Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile 90  
 80 85  
 Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe 105  
 95 100  
 Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile 120  
 110 115  
 His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe 135  
 125 130  
 Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr 150  
 140 145



His Leu Leu Leu Pro Cys Leu Lys Ala Cys Ala Pro Ser Arg Val  
 155 160 165  
 Val Val Val Ala Ser Ala Ala His Cys Arg Gly Arg Leu Asp Phe  
 170 175 180  
 Lys Arg Leu Asp Arg Pro Val Val Gly Trp Arg Gln Glu Leu Arg  
 185 190 195  
 Ala Tyr Ala Asp Thr Lys Leu Ala Asn Val Leu Phe Ala Arg Glu  
 200 205 210  
 Leu Ala Asn Gln Leu Glu Ala Thr Gly Val Thr Cys Tyr Ala Ala  
 215 220 225  
 His Pro Gly Pro Val Asn Ser Glu Leu Phe Leu Arg His Val Pro  
 230 235 240  
 Gly Trp Leu Arg Pro Leu Leu Arg Pro Leu Ala Trp Leu Val Leu  
 245 250 255  
 Arg Ala Pro Arg Gly Gly Ala Gln Thr Pro Leu Tyr Cys Ala Leu  
 260 265 270  
 Gln Glu Gly Ile Glu Pro Leu Ser Gly Arg Tyr Phe Ala Asn Cys  
 275 280 285  
 His Val Glu Glu Val Pro Pro Ala Ala Arg Asp Asp Arg Ala Ala  
 290 295 300  
 His Arg Leu Trp Glu Ala Ser Lys Arg Leu Ala Gly Leu Gly Pro  
 305 310 315  
 Gly Glu Asp Ala Glu Pro Asp Glu Asp Pro Gln Ser Glu Asp Ser  
 320 325 330  
 Glu Ala Pro Ser Ser Leu Ser Thr Pro His Pro Glu Glu Pro Thr  
 335 340 345  
 Val Ser Gln Pro Tyr Pro Ser Pro Gln Ser Ser Pro Asp Leu Ser  
 350 355 360  
 Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln  
 365 370 375

Leu Ser

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

cttcattggcc ttggacttgg ccag 24

<210> 208  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 208  
acgccagtgg cctcaagctg gttg 24

<210> 209  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 209  
ctttctgagc tctgagccac gtttgacat cctcatccac aatgc 45

<210> 210  
<211> 3716  
<212> DNA  
<213> Homo sapiens

<400> 210  
ggaggagaca gcctcctggg gggcaggggt tccctgcctc tgctgctcct 50  
gctcatcatg ggaggcatgg ctgaggactc cccgccccag atcctagtcc 100  
acccccagga ccagctgttc cagggccctg gccctgccag gatgagctgc 150  
caagcctcag gccagccacc tcccaccatc cgctgggtgc tgaatgggca 200  
gccctgagc atggtgcccc cagaccacaca ccacctcctg cctgatggga 250  
cccttctgct gctacagccc cctgcccggg gacatgcca cgatggccag 300  
gccctgtcca cagacctggg tgtctacaca tgtgaggcca gcaaccggct 350  
tggcacggca gtcagcagag gcgctcggct gtctgtggct gtccctccgg 400  
aggatttcca gatccagcct cgggacatgg tggctgtggt gggtgagcag 450  
tttactctgg aatgtgggcc gccctggggc caccagagc ccacagtctc 500  
atggtggaaa gatgggaaac ccctggccct ccagcccga aggcacacag 550  
tgtccggggg gtccctgctg atggcaagag cagagaagag tgacgaaggg 600  
acctacatgt gtgtggccac caacagcgca ggacataggg agagccgcgc 650  
agcccgggtt tccatccagg agccccagga ctacacggag cctgtggagc 700  
ttctggctgt gcgaattcag ctggaaaatg tgacactgct gaaccggat 750

cctgcagagg gcccgaagcc tagaccggcg gtgtggctca gctggaaggt 800  
cagtggccct gctgcgcctg cccaatctta cacggccttg ttcaggaccc 850  
agactgcccc gggaggccag ggagctccgt gggcagagga gctgctggcc 900  
ggctggcaga ggcagagct tggaggcctc cactggggcc aagactacga 950  
gttcaaagtg agaccatcct ctggccgggc tcgaggccct gacagcaacg 1000  
tgtgtctcct gaggtgccc gaaaaagtgc ccagtgcccc acctcaggaa 1050  
gtgactctaa agcctggcaa tggcactgtc tttgtgagct gggccccacc 1100  
acctgctgaa aaccacaatg gcatcatccg tggctaccag gtctggagcc 1150  
tgggcaacac atcactgcca ccagccaact ggactgtagt tggtagcag 1200  
accagctgg aaatcgccac ccatatgcca ggctcctact gcgtgcaagt 1250  
ggctgcagtc actggtgctg gagctgggga gccagtaga cctgtctgcc 1300  
tcctttttaga gcaggccatg gagcgagcca cccaagaacc cagtgagcat 1350  
ggtccttga ccttgagca gctgagggt accttgaagc ggctgaggt 1400  
cattgccacc tgcggtgttg cactctggct gctgcttctg ggcaccgccg 1450  
tgtgtatcca ccgccggcg cgagctaggg tgcacctggg cccaggtctg 1500  
tacagatata ccagtgagga tgccatccta aaacacagga tggatcacag 1550  
tgactcccag tggttggcag acaactggcg ttcacacctt ggctctcggg 1600  
acctgagcag cagcagcagc ctcagcagtc ggctgggggc ggatgcccgg 1650  
gaccactag actgtcgtcg ctcttgctc tcctgggact cccgaagccc 1700  
cggcgtgccc ctgcttcag acaccagcac tttttatggc tccctcatcg 1750  
ctgagctgcc ctccagtacc ccagccaggc caagtcccca ggtccagct 1800  
gtcaggcgcc tcccaccca gctggcccag ctctccagcc cctgttccag 1850  
ctcagacagc ctctgcagcc gcaggggact ctcttctccc cgcttgtctc 1900  
tggccctgc agaggcttg aaggccaaa agaagcagga gctgcagcat 1950  
gccaacagtt cccactgct cggggcagc cactccttg agctccgggc 2000  
ctgtgagtta ggaaatagag gttccaagaa cttttccaa agcccaggag 2050  
ctgtgcccc aactctggt gcctggcggg cctgggacc gaaactctc 2100  
agctcctcaa atgagctggt tactcgtcat ctccctccag caccctctt 2150  
tcctcatgaa actccccaa ctcagagtca acagaccag cctccggtg 2200

caccacagge tccctcctcc atcctgctgc cagcagcccc catccccatc 2250  
 cttagcccct gcagtcccc tagccccag gcctcttccc tctctggccc 2300  
 cagcccagct tccagtgcgc tgtccagctc ctactgtca tccctggggg 2350  
 aggatcaaga cagcgtgctg acccctgagg aggtagccct gtgcttgga 2400  
 ctcaagtgagg gtgaggagac tcccaggaac agcgtctctc ccatgccaa 2450  
 ggctccttca cccccacca cctatgggta catcagcgtc ccaacagcct 2500  
 cagagttcac ggacatgggc aggactggag gagggtggg gcccaagggg 2550  
 ggagtcttgc tgtgccacc tcggccctgc ctaccccca ccccagcga 2600  
 gggctcctta gccaatggtt ggggctcagc ctctgaggac aatgccgcca 2650  
 gcgccagagc cagccttgct agctcctccg atggctcctt cctcgtgat 2700  
 gctcactttg cccgggccct ggcagtggct gtggatagct ttggttccg 2750  
 tctagagccc agggaggcag actgcgtctt catagatgcc tcatcacctc 2800  
 cctccccacg ggatgagatc ttcctgacct ccaacctctc cctgccctg 2850  
 tgggagtgga ggccagactg gttggaagac atggaggtca gccacacca 2900  
 gcggctggga aggggatgc ctccctggc ccctgactct cagatctctt 2950  
 cccagagaag tcagctccac tgcgtatgc ccaaggctgg tcttctct 3000  
 gtgattact cctgaaccgt gtccctgaga cttcccagac gggaatcaga 3050  
 accacttctc ctgtccacct acaagacctg ggctgtggtg tgtgggtctt 3100  
 ggctgtgtt tctctgcagc tgggtccac cttccaagc ctccagagag 3150  
 ttctccctcc acgattgtga aaacaaatga aaacaaaatt agagcaaagc 3200  
 tgacctggag ccctcaggga gaaaacatc atctccacct gactcctagc 3250  
 cactgcttcc tctctgtgc catccactcc caccaccagg ttgttttggc 3300  
 ctgaggagca gccctgcctg ctgctcttcc cccaccattt ggatcacagg 3350  
 aagtggagga gccagaggtg cttttgtgga ggacagcagt ggctgctggg 3400  
 agagggtgt ggaggaagga gcttctcgga gcccctctc agccttacct 3450  
 gggccctcc tctagagaag agctcaactc tctccaacc tcacatgga 3500  
 aagaaaataa ttatgaatgc cactgaggca ctgaggccct acctcatgcc 3550  
 aaacaaaggg ttcaaggctg ggtctagcga ggatgctgaa ggaaggagg 3600  
 tatgagaccg taggtcaaaa gcaccatcct cgtactgttg tcaatgatg 3650

cttaagaaat ttgataccat aaaatggtaa aaaaaaaaaa aaaaaaaaaa 3700

aaaaaaaaaa aaaaaa 3716

<210> 211

<211> 985

<212> PRT

<213> Homo sapiens

<400> 211

Met Gly Gly Met Ala Gln Asp Ser Pro Pro Gln Ile Leu Val His  
1 5 10 15

Pro Gln Asp Gln Leu Phe Gln Gly Pro Gly Pro Ala Arg Met Ser  
20 25 30

Cys Gln Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg Trp Leu Leu  
35 40 45

Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His His Leu  
50 55 60

Leu Pro Asp Gly Thr Leu Leu Leu Leu Gln Pro Pro Ala Arg Gly  
65 70 75

His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr  
80 85 90

Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly  
95 100 105

Ala Arg Leu Ser Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln  
110 115 120

Pro Arg Asp Met Val Ala Val Val Gly Glu Gln Phe Thr Leu Glu  
125 130 135

Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp  
140 145 150

Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val  
155 160 165

Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu  
170 175 180

Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu  
185 190 195

Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr  
200 205 210

Glu Pro Val Glu Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val  
215 220 225

Thr Leu Leu Asn Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro  
230 235 240

TOH20T=H202T00T

Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala  
245 250 255

Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly  
260 265 270

Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser  
275 280 285

Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys  
290 295 300

Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val  
305 310 315

Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln  
320 325 330

Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp  
335 340 345

Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr  
350 355 360

Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp  
365 370 375

Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met  
380 385 390

Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly  
395 400 405

Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala  
410 415 420

Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr  
425 430 435

Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala  
440 445 450

Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val  
455 460 465

Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly  
470 475 480

Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met  
485 490 495

Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr  
500 505 510

Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg  
515 520 525

Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu

	530	535	540
Leu Ser Trp Asp	Ser Arg Ser Pro Gly	Val Pro Leu Leu Pro Asp	555
	545	550	
Thr Ser Thr Phe	Tyr Gly Ser Leu Ile	Ala Glu Leu Pro Ser Ser	570
	560	565	
Thr Pro Ala Arg	Pro Ser Pro Gln Val	Pro Ala Val Arg Arg Leu	585
	575	580	
Pro Pro Gln Leu	Ala Gln Leu Ser Ser	Pro Cys Ser Ser Ser Asp	600
	590	595	
Ser Leu Cys Ser	Arg Arg Gly Leu Ser	Ser Pro Arg Leu Ser Leu	615
	605	610	
Ala Pro Ala Glu	Ala Trp Lys Ala Lys	Lys Lys Gln Glu Leu Gln	630
	620	625	
His Ala Asn Ser	Ser Pro Leu Leu Arg	Gly Ser His Ser Leu Glu	645
	635	640	
Leu Arg Ala Cys	Glu Leu Gly Asn Arg	Gly Ser Lys Asn Leu Ser	660
	650	655	
Gln Ser Pro Gly	Ala Val Pro Gln Ala	Leu Val Ala Trp Arg Ala	675
	665	670	
Leu Gly Pro Lys	Leu Leu Ser Ser Ser	Asn Glu Leu Val Thr Arg	690
	680	685	
His Leu Pro Pro	Ala Pro Leu Phe Pro	His Glu Thr Pro Pro Thr	705
	695	700	
Gln Ser Gln Gln	Thr Gln Pro Pro Val	Ala Pro Gln Ala Pro Ser	720
	710	715	
Ser Ile Leu Leu	Pro Ala Ala Pro Ile	Pro Ile Leu Ser Pro Cys	735
	725	730	
Ser Pro Pro Ser	Pro Gln Ala Ser Ser	Leu Ser Gly Pro Ser Pro	750
	740	745	
Ala Ser Ser Arg	Leu Ser Ser Ser Ser	Leu Ser Ser Leu Gly Glu	765
	755	760	
Asp Gln Asp Ser	Val Leu Thr Pro Glu	Glu Val Ala Leu Cys Leu	780
	770	775	
Glu Leu Ser Glu	Gly Glu Glu Thr Pro	Arg Asn Ser Val Ser Pro	795
	785	790	
Met Pro Arg Ala	Pro Ser Pro Pro Thr	Thr Tyr Gly Tyr Ile Ser	810
	800	805	
Val Pro Thr Ala	Ser Glu Phe Thr Asp	Met Gly Arg Thr Gly Gly	825
	815	820	

Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro  
830 835 840

Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp  
845 850 855

Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu  
860 865 870

Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala  
875 880 885

Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu  
890 895 900

Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro  
905 910 915

Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro  
920 925 930

Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser  
935 940 945

His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp  
950 955 960

Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro  
965 970 975

Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser  
980 985

<210> 212  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 212  
gaaggacct acatgtgtgt ggcc 24

<210> 213  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 213  
actgaccttc cagctgagcc acac 24

<210> 214  
<211> 50  
<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 214

aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215

<211> 2749

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1869, 1887

<223> unknown base

<400> 215

ctccacaggt gtccagcgcc cagaatgcgg cttctgggcc tgctatgggg 50

ttgcctgtctg ctccaggtt atgaagccct ggaggggccca gaggaaatca 100

gcgggttcga aggggacact gtgtccctgc agtgcaccta cagggaagag 150

ctgagggacc accggaagta ctggtgcagg aagggtggga tctctttctc 200

tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250

agggcagggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300

accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtgggg 350

cgaaaaacgg ggccccgatg agtctttact gatctctctg ttctgtcttc 400

caggaccctg ctgtctctcc tccccttctc ccaccttcca gcctctggct 450

acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccagg 500

attgacttct cctgggctct acccggcagc caccacagcc aagcagggga 550

agacaggggc tgaggcccct ccattgccag ggacttccca gtacgggcac 600

gaaaggactt ctcaqtacac aggaacctct cctcaccag cgacctctcc 650

tctgcaggg agtcccgc ccccatgca gctggactcc acctcagcag 700

aggacaccag tccagctctc agcagtggca gctctaagcc cagggtgtcc 750

atcccgatgg tccgcatact ggccccagtc ctggtgctgc tgagccttct 800

gtcagccgca ggctgatcg cttctgcag ccacctgctc ctgtggagaa 850

aggaagctca acaggccacg gagacacaga ggaacgagaa gttctggctc 900

tcacgcttga ctgcggagga aaaggaagcc ccttcccagg cccctgaggg 950

ggacgtgatc tcgatgcctc ccttcacac atctgaggag gagctgggct 1000



agagttgttc agtatgcaaa acttggaag atggaggaga aaaagaaaag 2500  
 gaagaaaaaa atgtcaccca tagtctcacc agagactatc attatttcgt 2550  
 tttgtgttac ttccttcac tctttcttc ttcacataat ttgccggtgt 2600  
 tctttttaca gagcaattat cttgtatata caactttgta tctgccttt 2650  
 tccaccttat cgttccatca ctttattcca gcacttctct gtgttttaca 2700  
 gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaa 2749

<210> 216  
 <211> 332  
 <212> PRT  
 <213> Homo sapiens

<400> 216  
 Met Arg Leu Leu Val Leu Leu Trp Gly Cys Leu Leu Leu Pro Gly  
 1 5 10 15  
 Tyr Glu Ala Leu Glu Gly Pro Glu Glu Ile Ser Gly Phe Glu Gly  
 20 25 30  
 Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp  
 35 40 45  
 His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg  
 50 55 60  
 Cys Ser Gly Thr Ile Tyr Ala Glu Glu Glu Gly Gln Glu Thr Met  
 65 70 75  
 Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu  
 80 85 90  
 Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr  
 95 100 105  
 Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile  
 110 115 120  
 Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser  
 125 130 135  
 Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala  
 140 145 150  
 Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu  
 155 160 165  
 Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu  
 170 175 180  
 Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr  
 185 190 195  
 Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro

200	205	210
Ala Gly Ser Ser Arg Pro Pro Met Gln	Leu Asp Ser Thr Ser Ala	
215	220	225
Glu Asp Thr Ser Pro Ala Leu Ser Ser	Gly Ser Ser Lys Pro Arg	
230	235	240
Val Ser Ile Pro Met Val Arg Ile Leu	Ala Pro Val Leu Val Leu	
245	250	255
Leu Ser Leu Leu Ser Ala Ala Gly Leu	Ile Ala Phe Cys Ser His	
260	265	270
Leu Leu Leu Trp Arg Lys Glu Ala Gln	Gln Ala Thr Glu Thr Gln	
275	280	285
Arg Asn Glu Lys Phe Trp Leu Ser Arg	Leu Thr Ala Glu Glu Lys	
290	295	300
Glu Ala Pro Ser Gln Ala Pro Glu Gly	Asp Val Ile Ser Met Pro	
305	310	315
Pro Leu His Thr Ser Glu Glu Glu Leu	Gly Phe Ser Lys Phe Val	
320	325	330
Ser Ala		

<210> 217  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 217  
 ccctgcagtgcacctacagggaag 24

<210> 218  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 218  
 ctgtcttcccctgcttggtgtgg 24

<210> 219  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 219  
ggtgcaggaa ggggtgggata ctcttctctc gctgctctgg ccacatc 47

<210> 220  
<211> 950  
<212> DNA  
<213> Homo sapiens

<400> 220  
ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50  
ggggtggcag gagccgcaga gccagagcag acagccgaga aacagggtga 100  
cagtgtgaaa gaaccagtgg tctcgctctg ttgccaggc tagagtgtac 150  
tggcgtgata atagctcact gcagcctcag actcctggac ttgagaaatc 200  
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250  
cctgtttctt ctcttctgt gactggacca cggaggtctg tgagctgcct 300  
gtcatcccaa agctcagctc tgagccagag tgggtgtggc tccacctctg 350  
ccgccggcat agaagccagg agcagggtctc tcagaaggcg gtggtgccca 400  
gctgggatca tgttgttggc cctggtctgt ctgctcagct gcctgtacc 450  
ctccagttag gccaaactct acggtcgttg tgaactggcc agagtgtac 500  
atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550  
tgccttgctt atttcacaag cgttttcaac gcagctgctt tggactacga 600  
ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650  
ggtgcagcaa cctcaccctg aacgtcccca acgtgtgccg gatgtactgc 700  
tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750  
gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800  
actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850  
gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900  
cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221  
<211> 146  
<212> PRT  
<213> Homo sapiens

<400> 221  
Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser  
1 5 10 15  
Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu  
20 25 30

His Asp Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp  
 35 40 45  
 Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala  
 50 55 60  
 Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln  
 65 70 75  
 Ile Asn Ser Arg Arg Trp Cys Ser Asn Leu Thr Pro Asn Val Pro  
 80 85 90  
 Asn Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu  
 95 100 105  
 Lys Asp Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln  
 110 115 120  
 Gly Leu Gly Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys  
 125 130 135  
 Asp Leu Thr Glu Trp Val Asp Gly Cys Asp Phe  
 140 145

<210> 222  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 222  
 gggatcatgt tgttgccct ggtc 24

<210> 223  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 223  
 gcaaggcaga cccagtcagc cag 23

<210> 224  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 224  
 ctgcctgcta ccctccaagt. gaggccaagc tctacggtcg ttgtg 45

<210> 225

**THE UNIVERSITY OF CHICAGO**

155

gctgccactg accactcagt tggtatctgt gtccgttttt ctacttgcag 1400  
 acctaagggtg gagtaacaag gagtattacc accacatggc tactgaccgt 1450  
 gtcacgctggg aagagggggc cttatggcag ggaaaaatagg taccgacttg 1500  
 atggaagtca caccctctgg aaaaaagaac tcttaactct ccagcacaca 1550  
 tacacatgga ctcttggcag cttgagccta gaagccatgt ctctcaaag 1600  
 ccctgagaaa gggaacaagc agataccagg tcaagggcac cagggttcatt 1650  
 tcagccctta catggacagc tagaggttcg atatctgtgg gtccttcag 1700  
 gcaagaagag ggagatgaga gcaagagacg actgaagtcc caccctagaa 1750  
 cccagcctgc cccagcctgc ccctgggaag aggaaactta accactcccc 1800  
 agaccacct aggcaggcat ataggctgcc atcctggacc agggatccc 1850  
 gctgtgcctt tgcagtcag cccgagtcac ctttcacagc gctgttcctc 1900  
 catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950  
 acacacacac ggacacacac acacacctgc gagagagagg gaggaaagg 2000  
 ctgtgccttt gcagtcagc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226  
 <211> 351  
 <212> PRT  
 <213> Homo sapiens

<400> 226  
 Met Ser Pro Arg Ser Cys Leu Arg Ser Leu Arg Leu Leu Val Phe  
     1                    5                    10                    15  
 Ala Val Phe Ser Ala Ala Ala Ser Asn Trp Leu Tyr Leu Ala Lys  
                     20                    25                    30  
 Leu Ser Ser Val Gly Ser Ile Ser Glu Glu Glu Thr Cys Glu Lys  
                     35                    40                    45  
 Leu Lys Gly Leu Ile Gln Arg Gln Val Gln Met Cys Lys Arg Asn  
                     50                    55                    60  
 Leu Glu Val Met Asp Ser Val Arg Arg Gly Ala Gln Leu Ala Ile  
                     65                    70                    75  
 Glu Glu Cys Gln Tyr Gln Phe Arg Asn Arg Arg Trp Asn Cys Ser  
                     80                    85                    90  
 Thr Leu Asp Ser Leu Pro Val Phe Gly Lys Val Val Thr Gln Gly  
                     95                    100                    105  
 Thr Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser Ala Gly Val  
                     110                    115                    120



Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys
				125					130					135
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe
				140					145					150
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe
				155					160					165
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser
				170					175					180
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg
				185					190					195
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly
				200					205					210
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro
				215					220					225
Pro	Phe	Arg	Gln	Val	Gly	His	Ala	Leu	Lys	Glu	Lys	Phe	Asp	Gly
				230					235					240
Ala	Thr	Glu	Val	Glu	Pro	Arg	Arg	Val	Gly	Ser	Ser	Arg	Ala	Leu
				245					250					255
Val	Pro	Arg	Asn	Ala	Gln	Phe	Lys	Pro	His	Thr	Asp	Glu	Asp	Leu
				260					265					270
Val	Tyr	Leu	Glu	Pro	Ser	Pro	Asp	Phe	Cys	Glu	Gln	Asp	Met	Arg
				275					280					285
Ser	Gly	Val	Leu	Gly	Thr	Arg	Gly	Arg	Thr	Cys	Asn	Lys	Thr	Ser
				290					295					300
Lys	Ala	Ile	Asp	Gly	Cys	Glu	Leu	Leu	Cys	Cys	Gly	Arg	Gly	Phe
				305					310					315
His	Thr	Ala	Gln	Val	Glu	Leu	Ala	Glu	Arg	Cys	Ser	Cys	Lys	Phe
				320					325					330
His	Trp	Cys	Cys	Phe	Val	Lys	Cys	Arg	Gln	Cys	Gln	Arg	Leu	Val
				335					340					345
Glu	Leu	His	Thr	Cys	Arg									
				350										

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 228  
tggtagggaga ctgttttaaat tatcggcc 28

<210> 229  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 229  
tgcttcgtca agtgccggca gtgccagcgg ctctgtggagt t 41

<210> 230  
<211> 1355  
<212> DNA  
<213> Homo sapiens

<400> 230  
cggacgcgtg ggcggacgcg tgggaggacg cgtgggaggga cgcgtgggct 50  
gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggaggga 100  
gctccgagga ggtccccgga gggccctggg gacgctgggt gactggagc 150  
aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtctttg 200  
ggctgtgatt ctgagtatcc tattgtccaa ggcctccacg gaggcgcgg 250  
cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300  
gcggcgcgtg gtgccctgaa ggaggaggtc ggagactgcc acagctgctg 350  
ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400  
cgcaggcgaa gctgatggag caggagagcg cctgcggga actgcgtgag 450  
cgcgtgacct agggcttggc tgaagccggc aggggcccgtg aggacgtccg 500  
cactgagctg ttccggggcg tggaggccgt gaggctccag aacaactcct 550  
gcgagccgtg cccacgtcg tggtgtcct tcgagggtc ctgctacttt 600  
ttctctgtgc caaagacgac gtgggaggcg gcgcaggatc actgcgcaga 650  
tgccagcgcg cacctggtga tcgttggggg cctggatgag cagggttcc 700  
tcactcgaa cacgcgtggc cgtggttact ggctgggcct gagggtgtg 750

cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800  
cagcttcagc cactggaacc agggagagcc caatgacgct tgggggcgcg 850  
agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900  
gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950  
ccgcccagtg ccctggagcc ggcgccattg cagcatgtcg tatcctgggg 1000  
gtgtctcacc tccctggctc ctggagctga ttgccaaaga gtttttttct 1050  
tctcatcca ccgctgctga gtctcagaaa cacttggccc aacatagccc 1100  
tgtccagccc agtgccctggg ctctgggacc tccatgccga cctcatccta 1150  
actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200  
ctcctgcgtc cccgtgatat gcctccactt ctctccctaa ccaagggttag 1250  
gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300  
gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350  
aaaaa 1355

<210> 231  
<211> 293  
<212> PRT  
<213> Homo sapiens

<400> 231

Met	Asp	Thr	Thr	Arg	Tyr	Ser	Lys	Trp	Gly	Gly	Ser	Ser	Glu	Glu
1				5					10					15
Val	Pro	Gly	Gly	Pro	Trp	Gly	Arg	Trp	Val	His	Trp	Ser	Arg	Arg
				20					25					30
Pro	Leu	Phe	Leu	Ala	Leu	Ala	Val	Leu	Val	Thr	Thr	Val	Leu	Trp
				35					40					45
Ala	Val	Ile	Leu	Ser	Ile	Leu	Leu	Ser	Lys	Ala	Ser	Thr	Glu	Arg
				50					55					60
Ala	Ala	Leu	Leu	Asp	Gly	His	Asp	Leu	Leu	Arg	Thr	Asn	Ala	Ser
				65					70					75
Lys	Gln	Thr	Ala	Ala	Leu	Gly	Ala	Leu	Lys	Glu	Glu	Val	Gly	Asp
				80					85					90
Cys	His	Ser	Cys	Cys	Ser	Gly	Thr	Gln	Ala	Gln	Leu	Gln	Thr	Thr
				95					100					105
Arg	Ala	Glu	Leu	Gly	Glu	Ala	Gln	Ala	Lys	Leu	Met	Glu	Gln	Glu
				110					115					120
Ser	Ala	Leu	Arg	Glu	Leu	Arg	Glu	Arg	Val	Thr	Gln	Gly	Leu	Ala
				125					130					135

Glu Ala Gly Arg Gly Arg Glu Asp Val Arg Thr Glu Leu Phe Arg  
140 145 150

Ala Leu Glu Ala Val Arg Leu Gln Asn Asn Ser Cys Glu Pro Cys  
155 160 165

Pro Thr Ser Trp Leu Ser Phe Glu Gly Ser Cys Tyr Phe Phe Ser  
170 175 180

Val Pro Lys Thr Thr Trp Ala Ala Ala Gln Asp His Cys Ala Asp  
185 190 195

Ala Ser Ala His Leu Val Ile Val Gly Gly Leu Asp Glu Gln Gly  
200 205 210

Phe Leu Thr Arg Asn Thr Arg Gly Arg Gly Tyr Trp Leu Gly Leu  
215 220 225

Arg Ala Val Arg His Leu Gly Lys Val Gln Gly Tyr Gln Trp Val  
230 235 240

Asp Gly Val Ser Leu Ser Phe Ser His Trp Asn Gln Gly Glu Pro  
245 250 255

Asn Asp Ala Trp Gly Arg Glu Asn Cys Val Met Met Leu His Thr  
260 265 270

Gly Leu Trp Asn Asp Ala Pro Cys Asp Ser Glu Lys Asp Gly Trp  
275 280 285

Ile Cys Glu Lys Arg His Asn Cys  
290

<210> 232  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 232  
gcgagaactg tgatcatgatg ctgc 24

<210> 233  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 233  
gtttctgaga ctcagcagcg gtgg 24

<210> 234  
<211> 50  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gccaggggaa gagggtgatc cgacccgggg aaggtcgctg ggcagggcga 50

gttgggaaag cggcagcccc cgccgcccc gcagccctt ctcctccttt 100

ctcccacgtc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150

agacaggagg aactggagcc tcattggccg gccggggcg cgggcctcgg 200

gcttaaataag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250

cgctcccgt gtcctcgccg ggtgatgaa aacccagcc cggccgccgc 300

cctgggcaag gccctctcg ctctcctcct ggccactctc ggcgccgccg 350

gccagcctt tgggggagag tccatctgtt ccgccagagc cccggccaaa 400

tacagcatca cttcacggg caagtggagc cagacggcct tcccaagca 450

gtacccctg ttccgcccc ctgcgcagtg gtcttcgctg ctgggggccg 500

cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550

gggctgcgcg actttgcgga gcgcggcgag gcctggggcg tgatgaagga 600

gatcgaggcg gcgggggagg cgctgcagag cgtgcacgag gtgttttcgg 650

cgcccgcgt cccagcggc accgggcaga cgtcggcgga gctggagggtg 700

cagcgcaggc actcgctggt ctggtttgtg gtgcgcacgc tgcccagccc 750

cgactggttc gtgggcgtgg acagcctgga cctgtgcgac ggggaccgtt 800

ggcgggaaca ggcggcgctg gacctgtacc cctacgacgc cgggacggac 850

agcgggttca cttctctc ccccaacttc gccaccatcc cgcaggacac 900

ggtgaccgag ataacgtcct cctctcccag ccaccggcc aactccttct 950

actaccgcg gctgaaggcc ctgcctcca togccagggt gacactgctg 1000

cggctgcgac agagccccag ggcttcac cctccgccc cagtcctgcc 1050

cagcagggac aatgagattg tagacagcgc ctcaattcca gaaacgccgc 1100

1301001

tggactgcga ggtctccctg tggctgcctt ggggactgtg cggaggccac 1150  
 tgtgggagggc tcgggaccaa gagcaggact cgctacgtcc ggggccagcc 1200  
 cgccaacaac gggagcccct gccccgagct cgaagaagag gctgagtgcg 1250  
 tccctgataa ctgcgtctaa gaccagagcc ccgcagcccc tggggccccc 1300  
 cggagccatg ggggtgcggg ggctcctgtg caggctcatg ctgcaggcgg 1350  
 ccgagggcac aggggggttc gcgctgctcc tgaccgcggt gaggccgcgc 1400  
 cgaccatctc tgactgaag ggccctctgg tggccggcac gggcattggg 1450  
 aaacagcctc ctctttccc aaccttgctt cttaggggcc cccgtgtccc 1500  
 gtctgtctc agcctctcc tctgcagga taaagtcac cccaaggctc 1550  
 cagctactct aaattatgtc tcttataag ttattgtgc tccaggagat 1600  
 tgtccttcat cgtccagggg cctggctccc acgtggttg agatacctca 1650  
 gacctggtgc tctaggctgt gctgagccca ctctcccgag ggcgcatcca 1700  
 agcgggggcc acttgagaag tgaataaatg gggcggttcc ggaagcgtca 1750  
 gtgtttccat gttatggatc tctctgcgtt tgaataaaga ctatctctgt 1800  
 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 236  
 Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys  
 1 5 10 15  
 Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly  
 20 25 30  
 Gly Glu Ser Ile Cys Ser Ala Arg Ala Pro Ala Lys Tyr Ser Ile  
 35 40 45  
 Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr  
 50 55 60  
 Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala  
 65 70 75  
 Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val  
 80 85 90  
 Ser Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala  
 95 100 105  
 Leu Met Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val



<210> 238  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 238  
 caggactcgc tacgtccg 18  
  
 <210> 239  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 239  
 cagcccccttc tcctcctttc tccc 24  
  
 <210> 240  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 240  
 gcagttatca gggacgcact cagcc 25  
  
 <210> 241  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 241  
 ccagcgagag gcagatag 18  
  
 <210> 242  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 242  
 cggtcaccgt gtctgcggg atg 23  
  
 <210> 243  
 <211> 42  
 <212> DNA



aaaattaaaa aaggacacaa gtgcgaatgt taaatcagct ggagaaggag 1100

aagtggagaa	gaaatcagtc	agccgcagtg	aagagctcag	aaaagaagca	1150
agacaattaa	aacgggaact	cttagcagca	aaacaaaaaa	aagtagaaaa	1200
tgcagcaaaa	caagcagaaa	aaagaagtga	agaggaagaa	gccoctccag	1250
atggtgctgt	tgccgaatac	agaagagaaa	agcaaaagta	tgaagctttg	1300
aggaagcaac	agtcaaagaa	gggaacttcc	cgggaagatc	agacccttgc	1350
actgctgaac	cagtttaaat	ctaaactcac	tcaagcaatt	gctgaaacac	1400
ctgaaaatga	cattcctgaa	acagaagtag	aagatgatga	aggatggatg	1450
tcacatgtac	ttcagtttga	ggataaaaagc	agaaaagtga	aagatgcaag	1500
catgcaagac	tcagatacat	ttgaaatcta	tgatcctcgg	aatccagtga	1550
ataaaagaag	gaggggaagaa	agcaaaaagc	tgatgagaga	gaaaaaagaa	1600
agaagataaa	atgagaataa	tgataaccag	aacttgctgg	aaatgtgcct	1650
acaatggcct	tgtaacagcc	attgttccca	acagcatcac	ttaggggtgt	1700
gaaaagaagt	atttttgaac	ctgttgtctg	gttttgaaaa	acaattatct	1750
tgttttgcaa	attgtggaat	gatgtaagca	aatgcttttg	gttactggta	1800
catgtgtttt	ttcctagctg	acotttttata	ttgctaaatc	tgaataaaaa	1850
taacttttct	tccacaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaa	1894

<210> 245

<211> 472

<212> PRT

<213> Homo sapiens

<400> 245

Met Ser Asn Ile Tyr Ile.Gln Glu Pro Pro Thr Asn Gly Lys Val  
1 5 10 15

Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser  
20 25 30

Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu  
35 40 45

Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly  
50 55 60

Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly  
65 70 75

Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg  
80 85 90

Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly  
                    95                    100                    105

Ser	His	Asp	Asn	Gly	Ser	Gln	Phe	Phe	Phe	Thr	Leu	Gly	Arg	Ala	
				110					115					120	
Asp	Glu	Leu	Asn	Asn	Lys	His	Thr	Ile	Phe	Gly	Lys	Val	Thr	Gly	
				125					130					135	
Asp	Thr	Val	Tyr	Asn	Met	Leu	Arg	Leu	Ser	Glu	Val	Asp	Ile	Asp	
				140					145					150	
Asp	Asp	Glu	Arg	Pro	His	Asn	Pro	His	Lys	Ile	Lys	Ser	Cys	Glu	
				155					160					165	
Val	Leu	Phe	Asn	Pro	Phe	Asp	Asp	Ile	Ile	Pro	Arg	Glu	Ile	Lys	
				170					175					180	
Arg	Leu	Lys	Lys	Glu	Lys	Pro	Glu	Glu	Glu	Val	Lys	Lys	Leu	Lys	
				185					190					195	
Pro	Lys	Gly	Thr	Lys	Asn	Phe	Ser	Leu	Leu	Ser	Phe	Gly	Glu	Glu	
				200					205					210	
Ala	Glu	Glu	Glu	Glu	Glu	Glu	Val	Asn	Arg	Val	Ser	Gln	Ser	Met	
				215					220					225	
Lys	Gly	Lys	Ser	Lys	Ser	Ser	His	Asp	Leu	Leu	Lys	Asp	Asp	Pro	
				230					235					240	
His	Leu	Ser	Ser	Val	Pro	Val	Val	Glu	Ser	Glu	Lys	Gly	Asp	Ala	
				245					250					255	
Pro	Asp	Leu	Val	Asp	Asp	Gly	Glu	Asp	Glu	Ser	Ala	Glu	His	Asp	
				260					265					270	
Glu	Tyr	Ile	Asp	Gly	Asp	Glu	Lys	Asn	Leu	Met	Arg	Glu	Arg	Ile	
				275					280					285	
Ala	Lys	Lys	Leu	Lys	Lys	Asp	Thr	Ser	Ala	Asn	Val	Lys	Ser	Ala	
				290					295					300	
Gly	Glu	Gly	Glu	Val	Glu	Lys	Lys	Ser	Val	Ser	Arg	Ser	Glu	Glu	
				305					310					315	
Leu	Arg	Lys	Glu	Ala	Arg	Gln	Leu	Lys	Arg	Glu	Leu	Leu	Ala	Ala	
				320					325					330	
Lys	Gln	Lys	Lys	Val	Glu	Asn	Ala	Ala	Lys	Gln	Ala	Glu	Lys	Arg	
				335					340					345	
Ser	Glu	Glu	Glu	Glu	Ala	Pro	Pro	Asp	Gly	Ala	Val	Ala	Glu	Tyr	
				350					355					360	
Arg	Arg	Glu	Lys	Gln	Lys	Tyr	Glu	Ala	Leu	Arg	Lys	Gln	Gln	Ser	
				365					370					375	
Lys	Lys	Gly	Thr	Ser	Arg	Glu	Asp	Gln	Thr	Leu	Ala	Leu	Leu	Asn	
				380					385					390	
Gln	Phe	Lys	Ser	Lys	Leu	Thr	Gln	Ala	Ile	Ala	Glu	Thr	Pro	Glu	

395	400	405
Asn Asp Ile Pro Glu Thr Glu Val Glu	Asp Asp Glu Gly Trp Met	
410	415	420
Ser His Val Leu Gln Phe Glu Asp Lys	Ser Arg Lys Val Lys Asp	
425	430	435
Ala Ser Met Gln Asp Ser Asp Thr Phe	Glu Ile Tyr Asp Pro Arg	
440	445	450
Asn Pro Val Asn Lys Arg Arg Arg Glu	Glu Ser Lys Lys Leu Met	
455	460	465
Arg Glu Lys Lys Glu Arg Arg		
470		

<210> 246  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe  
 <400> 246  
 tgcggagatc ctactggcac aggg 24

<210> 247  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe  
 <400> 247  
 cgagttagtc agagcatg 18

<210> 248  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe  
 <400> 248  
 cagatggtgc tgttgccg 18

<210> 249  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 249  
 caactggaac aggaactgag atgtggatc 29  
  
 <210> 250  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 250  
 ctgggttcagc agtgcaaggg tctg 24  
  
 <210> 251  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 251  
 cctctccgat taaaacgc 18  
  
 <210> 252  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 252  
 gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45  
  
 <210> 253  
 <211> 2456  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 253  
 cgccgccggtt ggggctggaa gttcccgcga ggtccgtgcc gggcgagaga 50  
 gatgctgccc ggcccgcctc ggctttgagg cgagagaagt gtcccagacc 100  
 catttcgcct tgctgacggc gtcgagccct ggccagacat gtccacaggg 150  
 ttctccttcg ggtccgggac tctgggctcc accaccgtgg ccgccggcgg 200  
 gaccagcaca ggcggcggtt tctccttcgg aacgggaacg tctagcaacc 250  
 cttctgtggg gctcaatctt ggaaatcttg gaagtacttc aactccagca 300  
 actacatctg ctcttcaag tggttttgga accgggctct ttggatctaa 350  
 acctgccact gggttcactc taggaggaac aaatacaggt gccttgca 400



taagggtggc tatgcaggaa ggagccaaag aggggtttgc ccccaccatc 1900  
 caggccctgg ggagactagc catggacata cctggggaca agagttctac 1950  
 ccaccccagt ttagaactgc aggagctccc tgetgcctcc aggccaaagc 2000  
 tagagctttt gcctgttgtg tgggacctgc actgcccttt ccagcctgac 2050  
 atcccatgat gcccctctac ttcaactgtg acatccagtt aggccaggcc 2100  
 ctgtcaaac cacactgtgc tcagctctcc agcctcagga caacctcttt 2150  
 ttttcccttc ttcaaactct cccacccttc aatgtctcct tgtgactcct 2200  
 tcttatggga ggtcgaccca gactgccact gccctgtca ctgcaccag 2250  
 cttggcattt accatccatc ctgctcaacc ttgttcctgt ctgttcacat 2300  
 tggcctggag gcctagggca ggttgtgaca tggagcaaac ttttgtagt 2350  
 ttgggatctt ctctcccacc cacacttacc tccccaggg ccactccaaa 2400  
 gtctatacac aggggtggtc tcttcaataa agaagtgttg attagaaaaa 2450  
 aaaaaa 2456

<210> 254  
 <211> 545  
 <212> PRT  
 <213> Homo sapiens

<400> 254

Met	Ser	Thr	Gly	Phe	Ser	Phe	Gly	Ser	Gly	Thr	Leu	Gly	Ser	Thr
1				5					10					15
Thr	Val	Ala	Ala	Gly	Gly	Thr	Ser	Thr	Gly	Gly	Val	Phe	Ser	Phe
				20					25					30
Gly	Thr	Gly	Thr	Ser	Ser	Asn	Pro	Ser	Val	Gly	Leu	Asn	Phe	Gly
				35					40					45
Asn	Leu	Gly	Ser	Thr	Ser	Thr	Pro	Ala	Thr	Thr	Ser	Ala	Pro	Ser
				50					55					60
Ser	Gly	Phe	Gly	Thr	Gly	Leu	Phe	Gly	Ser	Lys	Pro	Ala	Thr	Gly
				65					70					75
Phe	Thr	Leu	Gly	Gly	Thr	Asn	Thr	Gly	Ala	Leu	His	Thr	Lys	Arg
				80					85					90
Pro	Gln	Val	Val	Thr	Lys	Tyr	Gly	Thr	Leu	Gln	Gly	Lys	Gln	Met
				95					100					105
His	Val	Gly	Lys	Thr	Pro	Ile	Gln	Val	Phe	Leu	Gly	Val	Pro	Phe
				110					115					120
Ser	Arg	Pro	Pro	Leu	Gly	Ile	Leu	Arg	Phe	Ala	Pro	Pro	Glu	Pro
				125					130					135

Pro Glu Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro  
140 145 150

Gly Trp Ser Leu Ala Leu Ser Pro Gly Trp Ser Ala Val Ala Arg  
155 160 165

Ser Arg Leu Thr Ala Thr Ser Ala Ser Arg Val Gln Ala Ser Leu  
170 175 180

Leu Pro Gln Pro Leu Ser Val Trp Gly Tyr Arg Cys Leu Gln Glu  
185 190 195

Ser Trp Gly Gln Leu Ala Ser Met Tyr Val Ser Thr Arg Glu Arg  
200 205 210

Tyr Lys Trp Leu Arg Phe Ser Glu Asp Cys Leu Tyr Leu Asn Val  
215 220 225

Tyr Ala Pro Ala Arg Ala Pro Gly Asp Pro Gln Leu Pro Val Met  
230 235 240

Val Trp Phe Pro Gly Gly Ala Phe Ile Val Gly Ala Ala Ser Ser  
245 250 255

Tyr Glu Gly Ser Asp Leu Ala Ala Arg Glu Lys Val Val Leu Val  
260 265 270

Phe Leu Gln His Arg Leu Gly Ile Phe Gly Phe Leu Ser Thr Asp  
275 280 285

Asp Ser His Ala Arg Gly Asn Trp Gly Leu Leu Asp Gln Met Ala  
290 295 300

Ala Leu Arg Trp Val Gln Glu Asn Ile Ala Ala Phe Gly Gly Asp  
305 310 315

Pro Gly Asn Val Thr Leu Phe Gly Gln Ser Ala Gly Ala Met Ser  
320 325 330

Ile Ser Gly Leu Met Met Ser Pro Leu Ala Ser Gly Leu Phe His  
335 340 345

Arg Ala Ile Ser Gln Ser Gly Thr Ala Leu Phe Arg Leu Phe Ile  
350 355 360

Thr Ser Asn Pro Leu Lys Val Ala Lys Lys Val Ala His Leu Ala  
365 370 375

Gly Cys Asn His Asn Ser Thr Gln Ile Leu Val Asn Cys Leu Arg  
380 385 390

Ala Leu Ser Gly Thr Lys Val Met Arg Val Ser Asn Lys Met Arg  
395 400 405

Phe Leu Gln Leu Asn Phe Gln Arg Asp Pro Glu Glu Ile Ile Trp  
410 415 420

Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro





<210> 258  
<211> 2764  
<212> DNA  
<213> Homo sapiens

<400> 258  
gagaacaggc ctgtctcagg caggccctgc gcctcctatg cggagatgct 50  
actgccactg ctgtctgcct cgctgctggg cgggtcccag gctatggatg 100  
ggagattctg gatacagagt caggagtcag tgatggtgcc ggagggcctg 150  
tgcattctctg tgccctgctc tttctcctac ccccgacaag actggacagg 200  
gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250  
aggggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300  
acccggggcc gattccagct cactggggat cccgccaagg ggaactgctc 350  
cttggtgatc agagacgcgc agatgcagga tgagtcacag tacttctttc 400  
gggtggagag aggaagctat gtgacatata atttcatgaa cgatgggttc 450  
tttctaaaag taacagtgtc cagcttcacg ccagacccc aggaccacaa 500  
caccgacctc acctgccatg tggacttctc cagaaagggt gtgagcgcac 550  
agaggaccgt ccgactcgt gtggcctatg ccccagaga ccttgttatc 600  
agcatttcac gtgacaacac gccagccctg gagccccagc ccaggggaaa 650  
tgtccatac ctggaagccc aaaaaggcca gttcctgcgg ctctctctgtg 700  
ctgtgacag ccagccccct gccacactga gctgggtcct gcagaacaga 750  
gtcctctcct cgtcccatcc ctggggccct agacccttg ggctggagct 800  
gcccggggtg aaggctggg attcaggcg ctacacctgc cgagcggaga 850  
acaggcttgg ctcccagcag cgagccctgg acctctctgt gcagtatcct 900  
ccagagaacc tgagagtgat ggtttcccaa gcaaacagga cagtctgga 950  
aaaccttggg aacggcacgt ctctcccagt actggagggc caaagcctgt 1000  
gcctggtctg tgtcacacac agcagcccc cagccaggt gagctggacc 1050  
cagaggggac aggttctgag cccctcccag ccctcagacc cgggggtcct 1100  
ggagctgcct cgggttcaag tgagcacga aggagagttc acctgccacg 1150  
ctcggcaccc actgggtcc cagcacgtct ctctcagcct ctccgtgcac 1200  
tataagaagg gactcatctc aacggcattc tccaacggag cgtttctggg 1250  
aatcggcatc acggtcttc tttctctctg cctggccctg atcatcatga 1300



tcaccttaaa aaaa 2764

<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln  
1 5 10 15

Ala Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met  
20 25 30

Val Pro Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr  
35 40 45

Pro Arg Gln Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp  
50 55 60

Phe Lys Ala Val Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr  
65 70 75

Asn His Gln Ser Arg Glu Val Glu Met Ser Thr Arg Gly Arg Phe  
80 85 90

Gln Leu Thr Gly Asp Pro Ala Lys Gly Asn Cys Ser Leu Val Ile  
95 100 105

Arg Asp Ala Gln Met Gln Asp Glu Ser Gln Tyr Phe Phe Arg Val  
110 115 120

Glu Arg Gly Ser Tyr Val Thr Tyr Asn Phe Met Asn Asp Gly Phe  
125 130 135

Phe Leu Lys Val Thr Val Leu Ser Phe Thr Pro Arg Pro Gln Asp  
140 145 150

His Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly  
155 160 165

Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro  
170 175 180

Arg Asp Leu Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Ala Leu  
185 190 195

Glu Pro Gln Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys  
200 205 210

Gly Gln Phe Leu Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro  
215 220 225

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser  
230 235 240

His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val  
245 250 255

TCACCTTAATAAAAA

Lys	Ala	Gly	Asp	Ser	Gly	Arg	Tyr	Thr	Cys	Arg	Ala	Glu	Asn	Arg	
				260					265					270	
Leu	Gly	Ser	Gln	Gln	Arg	Ala	Leu	Asp	Leu	Ser	Val	Gln	Tyr	Pro	
				275					280					285	
Pro	Glu	Asn	Leu	Arg	Val	Met	Val	Ser	Gln	Ala	Asn	Arg	Thr	Val	
				290					295					300	
Leu	Glu	Asn	Leu	Gly	Asn	Gly	Thr	Ser	Leu	Pro	Val	Leu	Glu	Gly	
				305					310					315	
Gln	Ser	Leu	Cys	Leu	Val	Cys	Val	Thr	His	Ser	Ser	Pro	Pro	Ala	
				320					325					330	
Arg	Leu	Ser	Trp	Thr	Gln	Arg	Gly	Gln	Val	Leu	Ser	Pro	Ser	Gln	
				335					340					345	
Pro	Ser	Asp	Pro	Gly	Val	Leu	Glu	Leu	Pro	Arg	Val	Gln	Val	Glu	
				350					355					360	
His	Glu	Gly	Glu	Phe	Thr	Cys	His	Ala	Arg	His	Pro	Leu	Gly	Ser	
				365					370					375	
Gln	His	Val	Ser	Leu	Ser	Leu	Ser	Val	His	Tyr	Lys	Lys	Gly	Leu	
				380					385					390	
Ile	Ser	Thr	Ala	Phe	Ser	Asn	Gly	Ala	Phe	Leu	Gly	Ile	Gly	Ile	
				395					400					405	
Thr	Ala	Leu	Leu	Phe	Leu	Cys	Leu	Ala	Leu	Ile	Ile	Met	Lys	Ile	
				410					415					420	
Leu	Pro	Lys	Arg	Arg	Thr	Gln	Thr	Glu	Thr	Pro	Arg	Pro	Arg	Phe	
				425					430					435	
Ser	Arg	His	Ser	Thr	Ile	Leu	Asp	Tyr	Ile	Asn	Val	Val	Pro	Thr	
				440					445					450	
Ala	Gly	Pro	Leu	Ala	Gln	Lys	Arg	Asn	Gln	Lys	Ala	Thr	Pro	Asn	
				455					460					465	
Ser	Pro	Arg	Thr	Pro	Pro	Pro	Pro	Gly	Ala	Pro	Ser	Pro	Glu	Ser	
				470					475					480	
Lys	Lys	Asn	Gln	Lys	Lys	Gln	Tyr	Gln	Leu	Pro	Ser	Phe	Pro	Glu	
				485					490					495	
Pro	Lys	Ser	Ser	Thr	Gln	Ala	Pro	Glu	Ser	Gln	Glu	Ser	Gln	Glu	
				500					505					510	
Glu	Leu	His	Tyr	Ala	Thr	Leu	Asn	Phe	Pro	Gly	Val	Arg	Pro	Arg	
				515					520					525	
Pro	Glu	Ala	Arg	Met	Pro	Lys	Gly	Thr	Gln	Ala	Asp	Tyr	Ala	Glu	
				530					535					540	
Val	Lys	Phe	Gln												

<210> 260  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 260  
caaagcctgc gcctggtctg tg 22

<210> 261  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 261  
ttctggagcc cagagggatg tgag 24

<210> 262  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 262  
ggagctgccca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263  
<211> 2857  
<212> DNA  
<213> Homo sapiens

<400> 263  
tgaagagtaa tagttggaat caaaagagtc aacgcaatga actgttat 50  
actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttgag 100  
caacagaaaa ctctcaaaac aagaaagtca agcagccagt gcgatctcat 150  
ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200  
aatgaatacg actagtcac acatcggcca gctaagatct gatttagaca 250  
atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300  
acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350  
tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400  
tcgctactgg aagggtgtg gaacctgagt ctgagtttgt catcaaagtt 450



gaaaacagat tctatttcct gagaaaagtg aagatttcag agagaatata 1950  
 ttccaatatg atgatgaagg gggtagagaa gaagatacag aggcctttga 2000  
 tatagcagag ctgaggagta gtaccataat gcgggaacgc aagactcgga 2050  
 aaaccacaag cgctgagatc aggagcctat acaggcagtc tttgcaagtt 2100  
 ggccccgaca gtgccatatt caggaaattc attctggaaa agctcgaaga 2150  
 agctaatact gatccgtgtg cccctccttt tgattccctc cagacctacg 2200  
 cttttgaggg aacagggtca ttagctggat cctgagctc cttagaatca 2250  
 gcagtctctg atcaggatga aagctatgat taccttaatg agttgggacc 2300  
 tcgctttaa agattagcat gcatgtttgg ttctgcagtg cagtcaaata 2350  
 attagggctt tttaccatca aaatttttaa aagtgcataa gtgtattcga 2400  
 acccaatggt agtcttaaag agttttgtgc cctggctcta tggcggggaa 2450  
 agccctagtc tatggagttt tctgatttcc ctggagtaaa tactccatgg 2500  
 ttattttaag ctacctacat gctgtcattg aacagagatg tggggagaaa 2550  
 tgtaaacaat cagctcacag gcatcaatac aaccagattt gaagtaaaat 2600  
 aatgtaggaa gatattaaaa gtagatgaga ggacacaaga tgtagtcgat 2650  
 ccttatgcga ttatattcatt atttacttag gaaagagtaa aaataccaaa 2700  
 cgagaaaatt taaaggagca aaaatttgca agtcaaataa aaatgtacaa 2750  
 atcgagataa catttacatt tctatcatat tgacatgaaa attgaaaatg 2800  
 tatagtcaga gaaattttca tgaattattc catgaagtat tgtttccttt 2850  
 atttaaa 2857

<210> 264

<211> 772

<212> PRT

<213> Homo sapiens

<400> 264

Met	Asn	Cys	Tyr	Leu	Leu	Leu	Arg	Phe	Met	Leu	Gly	Ile	Pro	Leu
1				5					10					15

Leu	Trp	Pro	Cys	Leu	Gly	Ala	Thr	Glu	Asn	Ser	Gln	Thr	Lys	Lys
				20					25					30

Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp
				35					40					45

Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser
				50					55					60



His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn	
				65					70					75	
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe	
				80					85					90	
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu	
				95					100					105	
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile	
				110					115					120	
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val	
				125					130					135	
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp	
				140					145					150	
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr	
				155					160					165	
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser	
				170					175					180	
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro	
				185					190					195	
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser	
				200					205					210	
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln	
				215					220					225	
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr	
				230					235					240	
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile	
				245					250					255	
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro	
				260					265					270	
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile	
				275					280					285	
Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser	
				290					295					300	
Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile	
				305					310					315	
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr	
				320					325					330	
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu	
				335					340					345	
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln	

350	355	360
Val Glu Asp Val Asp Glu Pro Pro Leu Phe Leu Leu Pro Tyr Tyr		
365	370	375
Val Phe Glu Val Phe Glu Glu Thr Pro Gln Gly Ser Phe Val Gly		
380	385	390
Val Val Ser Ala Thr Asp Pro Asp Asn Arg Lys Ser Pro Ile Arg		
395	400	405
Tyr Ser Ile Thr Arg Ser Lys Val Phe Asn Ile Asn Asp Asn Gly		
410	415	420
Thr Ile Thr Thr Ser Asn Ser Leu Asp Arg Glu Ile Ser Ala Trp		
425	430	435
Tyr Asn Leu Ser Ile Thr Ala Thr Glu Lys Tyr Asn Ile Glu Gln		
440	445	450
Ile Ser Ser Ile Pro Leu Tyr Val Gln Val Leu Asn Ile Asn Asp		
455	460	465
His Ala Pro Glu Phe Ser Gln Tyr Tyr Glu Thr Tyr Val Cys Glu		
470	475	480
Asn Ala Gly Ser Gly Gln Val Ile Gln Thr Ile Ser Ala Val Asp		
485	490	495
Arg Asp Glu Ser Ile Glu Glu His His Phe Tyr Phe Asn Leu Ser		
500	505	510
Val Glu Asp Thr Asn Asn Ser Ser Phe Thr Ile Ile Asp Asn Gln		
515	520	525
Asp Asn Thr Ala Val Ile Leu Thr Asn Arg Thr Gly Phe Asn Leu		
530	535	540
Gln Glu Glu Pro Val Phe Tyr Ile Ser Ile Leu Ile Ala Asp Asn		
545	550	555
Gly Ile Pro Ser Leu Thr Ser Thr Asn Thr Leu Thr Ile His Val		
560	565	570
Cys Asp Cys Gly Asp Ser Gly Ser Thr Gln Thr Cys Gln Tyr Gln		
575	580	585
Glu Leu Val Leu Ser Met Gly Phe Lys Thr Glu Val Ile Ile Ala		
590	595	600
Ile Leu Ile Cys Ile Met Ile Ile Phe Gly Phe Ile Phe Leu Thr		
605	610	615
Leu Gly Leu Lys Gln Arg Arg Lys Gln Ile Leu Phe Pro Glu Lys		
620	625	630
Ser Glu Asp Phe Arg Glu Asn Ile Phe Gln Tyr Asp Asp Glu Gly		
635	640	645

Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Glu Leu Arg  
650 655 660

Ser Ser Thr Ile Met Arg Glu Arg Lys Thr Arg Lys Thr Thr Ser  
665 670 675

Ala Glu Ile Arg Ser Leu Tyr Arg Gln Ser Leu Gln Val Gly Pro  
680 685 690

Asp Ser Ala Ile Phe Arg Lys Phe Ile Leu Glu Lys Leu Glu Glu  
695 700 705

Ala Asn Thr Asp Pro Cys Ala Pro Pro Phe Asp Ser Leu Gln Thr  
710 715 720

Tyr Ala Phe Glu Gly Thr Gly Ser Leu Ala Gly Ser Leu Ser Ser  
725 730 735

Leu Glu Ser Ala Val Ser Asp Gln Asp Glu Ser Tyr Asp Tyr Leu  
740 745 750

Asn Glu Leu Gly Pro Arg Phe Lys Arg Leu Ala Cys Met Phe Gly  
755 760 765

Ser Ala Val Gln Ser Asn Asn  
770

<210> 265  
<211> 349  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 24, 60, 141, 226, 228, 249, 252  
<223> unknown base

<400> 265  
atttcaaggc cagccatatt tttntgttga accaacaaca ggagtcataa 50  
gaatattttt taaaatggat agagaactgc aagatgagta ttgggtaatc 100  
attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150  
aagtgtatta attaaacttt cagatgttaa tgacaataag cctatatatta 200  
aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250  
tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300  
aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266  
<211> 25  
<212> DNA  
<213> Artificial Sequence  
<220>

<223> Synthetic oligonucleotide probe

<400> 266  
cttgactgtc tctgaatctg caccc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267  
aagtgtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268  
ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

gcaacctcag cttctagtat ccagactcca gcgccgcccc gggcgaggac 50  
cccaaccccc acccagagct tctccagcgg cggcgcagcg agcaggggtc 100  
cccgccctaa cttctccgc ggggccagc caccttcggg agtcggggtt 150  
gcccacctgc aaactctccg cttctgcac ctgccacccc tgagccagcg 200  
cgggcccccg agcgagtcac ggccaacgcg gggctgcagc tgttgggctt 250  
cattctcgcc ttctgggat ggatcggcgc catcgtcagc actgccctgc 300  
cccagtggag gatttactcc tatgccggcg acaacatcgt gaccgcccag 350  
gccatgtacg aggggctgtg gatgtcctgc gtgtcgcaga gcaccgggca 400  
gatccagtgc aaagtcttg actccttgct gaatctgagc agcacattgc 450  
aagcaaccog tgccttgatg gtggttgga tcctcctggg agtgatagca 500  
atctttgtgg ccaccgttg catgaagtgt atgaagtgt tggaagacga 550  
tgaggtgcag aagatgagga tggctgtcat tgggggtgcg atatttcttc 600



tttatattac tcttattctt tgaacatgaa ctatgcctat gtagtgtctt 2100  
 tatttgctca gctggctgag aactgaaga agtcactgaa caaacctac 2150  
 acacgtacct tcattgtgatt cactgccttc ctctctctac cagtctattt 2200  
 ccactgaaca aaacctacac acataccttc atgtggttca gtgccttcct 2250  
 ctctctacca gtctatttcc actgaacaaa acctacgcac ataccttcat 2300  
 gtggctcagt gccttctctt ctctaccagt ctatttccat tctttcagct 2350  
 gtgtctgaca tgtttggtct ctgttccatt ttaacaactg ctcttacttt 2400  
 tccagtctgt acagaatgct atttcacttg agcaagatga tgtaatggaa 2450  
 aggggtgttg cactggtgtc tggagacctg gatttgagtc ttggtgctat 2500  
 caatcaccgt ctgtgtttga gcaaggcatt tggctgctgt aagcttattg 2550  
 cttcatctgt aagcgggtgt ttgtaattcc tgatcttccc acctcacagt 2600  
 gatgttggtg ggatccagtg agatagaata catgtaagtg tggttttgta 2650  
 atttaaaaag tgctatacta agggaaagaa ttgaggaatt aactgcatac 2700  
 gttttggtgt tgcttttcaa atgtttgaaa ataaaaaaaa tgtaag 2747

<210> 270

<211> 211

<212> PRT

<213> Homo sapiens

<400> 270

Met	Ala	Asn	Ala	Gly	Leu	Gln	Leu	Leu	Gly	Phe	Ile	Leu	Ala	Phe
1				5					10					15
Leu	Gly	Trp	Ile	Gly	Ala	Ile	Val	Ser	Thr	Ala	Leu	Pro	Gln	Trp
				20					25					30
Arg	Ile	Tyr	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Val	Thr	Ala	Gln	Ala
				35					40					45
Met	Tyr	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Ser	Gln	Ser	Thr	Gly
				50					55					60
Gln	Ile	Gln	Cys	Lys	Val	Phe	Asp	Ser	Leu	Leu	Asn	Leu	Ser	Ser
				65					70					75
Thr	Leu	Gln	Ala	Thr	Arg	Ala	Leu	Met	Val	Val	Gly	Ile	Leu	Leu
				80					85					90
Gly	Val	Ile	Ala	Ile	Phe	Val	Ala	Thr	Val	Gly	Met	Lys	Cys	Met
				95					100					105
Lys	Cys	Leu	Glu	Asp	Asp	Glu	Val	Gln	Lys	Met	Arg	Met	Ala	Val
				110					115					120

Ile Gly Gly Ala	Ile Phe Leu Leu Ala	Gly Leu Ala Ile Leu Val
125		130 135
Ala Thr Ala Trp	Tyr Gly Asn Arg Ile Val Gln Glu Phe Tyr Asp	
140		145 150
Pro Met Thr Pro	Val Asn Ala Arg Tyr Glu Phe Gly Gln Ala Leu	
155		160 165
Phe Thr Gly Trp	Ala Ala Ala Ser Leu Cys Leu Leu Gly Gly Ala	
170		175 180
Leu Leu Cys Cys	Ser Cys Pro Arg Lys Thr Thr Ser Tyr Pro Thr	
185		190 195
Pro Arg Pro Tyr	Pro Lys Pro Ala Pro Ser Ser Gly Lys Asp Tyr	
200		205 210

Val

<210> 271  
 <211> 564  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 21, 69, 163, 434, 436, 444  
 <223> unknown base

<400> 271  
 ttctggccaa acccggggct ncagctgttg ggcttcatct cgccttctctg 50  
 ggatggatcg ggcctatcnt cacactgccc ttccccagtg gaggatttta 100  
 ctccctatgc tggcgacaac atcgtgaccg ccagagccat gtacgagggg 150  
 ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200  
 ctttgactcc ttgtgaatc tgagcagcac attgcaagca acccgtgcct 250  
 tgatggtggt tggcatctc ctgggagtga tagcaatctt tgtggccacc 300  
 gttggcatga agtgtatgaa gtgcttgaa gacgatgagg tgcagaagat 350  
 gaggatggct gtcattggg ggcgatatt tcttcttgca ggtctggcta 400  
 ttttagttgc cacagcatgg tatggcaata gaancttca acantttctat 450  
 gaccctatga cccagtcaa tgccaggtac gaatttggtc aggtctcttt 500  
 cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550  
 gctgttctctg tccc 564

<210> 272  
 <211> 498

<212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> unsure  
 <222> 30, 49, 102, 141, 147, 171, 324-325, 339-341  
 <223> unknown base  
 <400> 272  
 acccttgacc caacgcggcc ccccgaccgn ttcattggcca aacgcgggnc 50  
 tccagctggt gggcttcatt ctccccttcc tgggatggac cggcgcccat 100  
 cntcagcact gccctgcccc agtggaggat ttactcctat nccgcnaca 150  
 acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtcctgcgtg 200  
 tcgcagagca ccgggcagat ccagtgcaca gtctttgact cccttgctga 250  
 atctgagcag cacattgcaa gcaaccctg ccttgatggt ggttggcatc 300  
 ctctggggag tgatagcaat cttnttggcc accgttgttn ntgaagtga 350  
 tgaagtgcct ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400  
 gggggcgcca tatttcttct tgcaggtctg gctattttag ttgccacagc 450  
 atggtatggc aatagaatcg ttcaagaatt ctatgacct atgaccga 498  
 <210> 273  
 <211> 552  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> unsure  
 <222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394  
 <223> unknown base  
 <400> 273  
 gggcccgacc attatccaac cgggntcact gttggtcat ctccctcctg 50  
 gatgaancgc gccatcntca gactccctgc cccatggaga tttncctat 100  
 gctggcgaca acatcntgac cccagccat gtacgagggg ctttgaacgt 150  
 cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200  
 tgctgaatct gngcagcaca ttgcagcaac cntgcccctg atggtggttg 250  
 gcactcctct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300  
 tgtatgaagt gcttggaaga cgatgaggtg cagaagatga ggatggctgt 350  
 cattgggggc gcgatatttc ttcttgagg tctggctatt tnnngttgcc 400  
 acagcatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450



cccagtcaat gccaggtacg aatttgggtca ggctctcttc actgggtggg 500  
 ctgctgcttc tctctgcctt ctgggaggtg ccctactttg ctgttcctgc 550  
 ga 552

<210> 274  
 <211> 526  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407  
 <223> unknown base

<400> 274  
 attctcccct cctggatgga tcgcnccacc gtcacattgc cttccccan 50

tgaggattn actcctatgc tggcgacaac atcgtgaccc cccaggccat 100  
 ttaccgaggg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150  
 ccagtgc aaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200  
 caacccgtgc cttgatgggg ttggcatcct cctgggagtg atagcaacct 250  
 ttgtggccac cgttggcatg aagtgtatga agtgcttggg agacgatgag 300  
 gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttgttg 350  
 caggctctggc tattttagtn gccacagcat ggtatggcaa tagantnntt 400  
 cnngnnntct atgaccctat gacccagtc aatgccaggt acgaatttgg 450  
 tcaggtcttc ttcactggct gggctgctgc ttctctctgc cttctgggag 500  
 gtgccctact ttgctgttcc tgtccc 526

<210> 275  
 <211> 398  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274  
 <223> unknown base

<400> 275  
 agagcaccgg cagatcccag tncaaagtct ttgacccttg ctgaatctga 50  
 gcagcacatt ncaagcaacc ccttgcccttg aagggtggtg ncatcccccc 100  
 tgggagtga tagcaatctt tgtggccacc gttggcatga agtntatgaa 150  
 gtgcttgga gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250  
 tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtc aa 300  
 tgccaggtag gaatttggtc aggtctctct cactggctgg gctgctgctt 350  
 ctctctgcct tctgggaggt gccctacttt gctgttctctg tccccgaa 398

<210> 276  
 <211> 495  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476  
 <223> unknown base

<400> 276  
 agcaatgccc tgccccaggt ggaggattaa ttcctatgnt ggggacaaca 50  
 ttgtgacngc ccaggccatg tacggggggc tgtggatgtc ctgctgtctg 100  
 cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150  
 gagcagcaca ttgcaagcaa cccgtgcctt gatggtgggt ggcatcttcc 200  
 tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250  
 tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300  
 cgcgatattt ctntttgcag gtctggctat tttagttgcc acagcatggt 350  
 atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400  
 gccaggtagc aatttggtca ggctttnttc actggctggg ctgctgcttn 450  
 tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277  
 <211> 200  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 34, 87, 138, 147, 163, 165-166, 172  
 <223> unknown base

<400> 277  
 tcataggggg gcgcgatatt ttttcttgca ggtntggtta ttttagttgc 50  
 cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100  
 cccagtc aa tgccaggtag gaatttggtc aggtctntt cactggntgg 150  
 gctgctgctt ctntnngcct ntgggaggt gccctacttt gctgttctctg 200

<210> 278  
<211> 542  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396  
<223> unknown base

<400> 278  
ttcctgggat ggatccgccc ccatactcac atgccctgcc ccttgagat 50  
ttacnccat gctggcgaac aacatctga ccgccaggc catgtacgag 100  
gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtgc 150  
aagtctttga ctcccttgctg aatctgagca gcacattgca agcaaccntg 200  
ccttgatggt ggttggcatc ctccctgggag tgatagcaat ctttgtggcc 250  
accgttggca tgaaagtga tgaagtgtt ggaagacgat gaggtgcaga 300  
agatgaggat ggctgtcatt gggggcgca tatttcttct tgcaggtctg 350  
gctattttag nngccacagc atggtatggc aatcagaccc nntcanaaac 400  
tctatgacc tatgaccca gtcaatgcca ggtacgaatt tggtcaggct 450  
ctcttcaactg gctgggctgc tgcttctctc tgccttcttg gaggtgccct 500  
actttgctgt tcctgtcccc gaaaaacaac ctcttaccga cg 542

<210> 279  
<211> 548  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 90, 115, 147, 228, 387  
<223> unknown base

<400> 279  
cggggctgca gctgttgggc ttcatctcgc ttccctgggat ggaatcggcg 50  
ccatcgctcag cactgccctg ccccatggag gatttactcn tatgtggcg 100  
acaacatcgt gaccncccag gccatgtacg aggggctgtg gatgtcngcg 150  
tgtcgcagag caccgggcag atccagtgc aagtctttga ctcccttgctg 200  
aatctgagca gcacattgca agcaaccntg ccttgatggt ggttggcatc 250  
ctccctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300  
gaagtgttg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350

ggggcgcgat atttcttctt gcaggctctgg ctatttntag ttgccacagc 400  
 atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450  
 tcaatgccag gtacgaattt ggtcaggctc tcttcactgg ctgggctgct 500  
 gcttctctct gccttctggg aggtgcccta ctttgctgtt cctgcgaa 548

<210> 280  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 280  
 cgagcgagtc atggccaacg c 21

<210> 281  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 281  
 gtgtcacacg tagtctttcc cgctgg 26

<210> 282  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 282  
 ctgcagctgt tgggcttcat tctgccttc ctgggatgga tcg 43

<210> 283  
 <211> 2285  
 <212> DNA  
 <213> Homo sapiens

<400> 283  
 gcgtgccgtc agctcgccgg gcaccgcggc ctgcgcctcg cctccgccc 50  
 ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gccacccgg 100  
 tagaggaccc ccgcccgtgc ccgaccggt cccgccttt ttgtaaaact 150  
 taaagcgggc gcagcattaa cgcttcccgc cccggtgacc tctcaggggt 200  
 ctccccgcca aaggtgctcc gccgctaagg aacatggcga aggtggagca 250  
 ggtcctgagc ctgcagccgc agcacgagct caaattccga ggtcccttca 300

ccgatgttgt caccaccaac ctaaagcttg gcaacccgac agaccgaaat 350  
 gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400  
 caacagcgga atcatcgatg caggggcctc aattaatgta tctgtgatgt 450  
 tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500  
 gttcagtcta tgtttgctcc aactgacact tcagatatgg aagcagtatg 550  
 gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600  
 ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650  
 attatatcca caactgcatc aaagacagaa acaccaatag tgtctaagtc 700  
 tctgagttct tctttggatg acaccgaagt taagaagggt atggaagaat 750  
 gtaagaggct gcaaggtgaa gttcagaggc tacgggagga gaacaagcag 800  
 ttcaaggaag aagatggact gcgatgagg aagacagtgc agagcaacag 850  
 ccccatattca gcattagccc caactgggaa ggaagaaggc cttagcacc 900  
 ggctcttgcc tctggtggtt ttgttcttta tcgttggtgt aattattggg 950  
 aagattgcct tgtagaggta gcatgcacag gatggtaa at tggattggtg 1000  
 gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050  
 aattaatgta tgatgacatc tcacaggtct tgcctttaa ttaccctcc 1100  
 ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150  
 ttagaaagt aaataatgtat agtaactgat tgagggggaa aaagaatgat 1200  
 ctttattaat gacaaggga accatgagta atgccacaat ggcatattgt 1250  
 aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300  
 tctcttaaaa tgacaccctt cctgcctgt tgggtgctggc ccttggggag 1350  
 ctggagccca gcatgctggg gagtgcggtc agctccacac agtagtcccc 1400  
 acgtggccca ctcccgccc aggtgcttt cgtgtcttc agttctgtcc 1450  
 aagccatcag ctcttgga ctgatgaaca gagtcaag cccaaaggaa 1500  
 ttgactgtg gcagcatcag acgtactcgt cataagtga aggcgtgtgt 1550  
 tgactgattg acccagcgt ttgaaataa atggcagtgc tttgttact 1600  
 taaagggacc aagctaaatt tgtattggt catgtagtga agtcaaactg 1650  
 ttattcagag atgtttaatg catatttaac ttatttaatg tatttcatt 1700  
 catgtttct tattgtcaca agagtacagt taatgctgcg tgctgctgaa 1750

ctctgttggg tgaactggta ttgctgctgg agggctgtgg gctcctctgt 1800  
 ctctggagag tctgggtcatg tggaggtggg gtttattggg atgctggaga 1850  
 agagctgccca ggaagtgttt tttctgggtc agtaaataac aactgtcata 1900  
 gggagggaaa ttctcagtag tgacagtcaa ctctaggtta ccttttttaa 1950  
 tgaagagtag tcagtcttct agattgttct tataccacct ctcaaccatt 2000  
 actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050  
 ggacctagcc tggagtcagg acaaatggat cgggctgcag agggtttagaa 2100  
 gcgagggcac cagcagttgt ggggtggggag caaggaaga gagaaactct 2150  
 tcagcgaatc cttctagtac tagttgagag ttgactgtg aattaatttt 2200  
 atgccataaa agaccaaccc agttctgttt gactatgtag catcttgaâa 2250  
 agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400

<210> 284  
 <211> 243  
 <212> PRT  
 <213> Homo sapiens  
 <400> 284  
 Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu  
 1 5 10 15  
 Leu Lys Phe Arg Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu  
 20 25 30  
 Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys  
 35 40 45  
 Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile  
 50 55 60  
 Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro  
 65 70 75  
 Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val  
 80 85 90  
 Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val  
 95 100 105  
 Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg  
 110 115 120  
 Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val  
 125 130 135  
 Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr  
 140 145 150

Pro	Ile	Val	Ser	Lys	Ser	Leu	Ser	Ser	Ser	Leu	Asp	Asp	Thr	Glu
				155					160					165
Val	Lys	Lys	Val	Met	Glu	Glu	Cys	Lys	Arg	Leu	Gln	Gly	Glu	Val
				170					175					180
Gln	Arg	Leu	Arg	Glu	Glu	Asn	Lys	Gln	Phe	Lys	Glu	Glu	Asp	Gly
				185					190					195
Leu	Arg	Met	Arg	Lys	Thr	Val	Gln	Ser	Asn	Ser	Pro	Ile	Ser	Ala
				200					205					210
Leu	Ala	Pro	Thr	Gly	Lys	Glu	Glu	Gly	Leu	Ser	Thr	Arg	Leu	Leu
				215					220					225
Ala	Leu	Val	Val	Leu	Phe	Phe	Ile	Val	Gly	Val	Ile	Ile	Gly	Lys
				230					235					240

Ile Ala Leu

Footnote 430

<210> 285  
 <211> 418  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 40, 53, 68, 119, 134, 177-178, 255  
 <223> unknown base

<400> 285  
 gtcagtcttc tagattgtcc ttatcccacc ttccaaccan tactcacatt 50  
 tcnagcgccc aggtccangt ctgagcctga ctcccccttg gggacctagc 100  
 ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150  
 cagcagtttt ggggtggggag caagggngga gagaaactct tcagcgaatc 200  
 cttctagtag tagttgagag tttgactgtg aattaatttt atgccataaa 250  
 agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300  
 taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350  
 ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400  
 gttaacttta aaatgagc 418

<210> 286  
 <211> 543  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 73, 97

<223> unknown base  
 <400> 286  
 tattgtaaag gccattttaa accattggta ggccttggt catgatgctg 50  
 gattacctcc ttaaagaca ccnttcctcg cctgttggtg ctggccnttg 100  
 gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150  
 gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200  
 ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250  
 aaggaattgc cactgtggca gcatcagacg tactcgatcat aagtgaagg 300  
 cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350  
 gttcacttaa agggaccaag ctaaattgta ttggttcag tagtgaagtc 400  
 aaactgttat tcagagatgt ttaatgcata ttaacttat ttaatgtatt 450  
 tcatctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500  
 gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543  
 <210> 287  
 <211> 270  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> unsure  
 <222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242  
 <223> unknown base  
 <400> 287  
 ccctggtggt tttgttcttt aattcggttg tgtaattntt gggaagattg 50  
 cttgtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100  
 catatccatg ggatttaaat ttatcataac catgtgtaaa aagaaattaa 150  
 tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200  
 acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250  
 agttaaaaaat gtatagtaac 270  
 <210> 288  
 <211> 428  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> unsure  
 <222> 35, 116, 129, 197, 278, 294, 297, 349, 351  
 <223> unknown base



<400> 288  
 ggtggcccat tcccggccca ggctgctttc cggtnnttcag ttctgtccaa 50  
 gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100  
 gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150  
 actgattgac ccagcgcttt ggaaataaat ggcagtgtt tttcantta 200  
 aagggaccaa gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250  
 attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300  
 tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350  
 ntgttgggtg aactgggtatt gctgctggag ggctgtgggc tcctctgtct 400  
 ttggagagtc-tggcatgtg gaggtggg 428

<210> 289  
 <211> 320  
 <212> DNA  
 <213> Homo sapiens

<400> 289  
 tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50  
 atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100  
 tactcgtcat aagtgagagg cgtgtgttga ctgattgacc cagcgctttg 150  
 gaaataaatg gcagtgttt gtacacttaa agggaccaag cttaaattgt 200  
 attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250  
 atttaactta tttaatgtat ttcattctcat gttttcttat tgtcacaaga 300  
 gtacagttaa tgctgcgtgc 320

<210> 290  
 <211> 609  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,  
 447, 481, 513, 532, 584, 598  
 <223> unknown base

<400> 290  
 aaacctttaa aagttgagg gaaaagaatg atcctttatt aatgacaagg 50  
 gaaacntgn gtaatgccac aatggcatat tgtaaatgtc attttaaaca 100  
 ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150  
 cttcctcgcc tgttgggtgt ggcccttggg gagctngagc ccagcatgct 200



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcgggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

gcgagctccg ggtgctgtgg cccggccttg gcggggcggc ctccggctca 50

ggctggctga gaggtccca gctgcagcgt ccccgccgc ctctcgga 100

gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150

gtctcacttt gttgccagg ctggagttca gtgccatgat catggtttac 200

tgcagccttg acctctggg ttcaagcag cctgctgagt agctgggact 250

acaggacaaa attagaagat caaatggaa aatatgctgc ttgggttgat 300

atttttcacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350

attttatgtg gcacttgaga aaggtacccc ggattgtcag tgaaaggact 400

ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450

tacagtgtgt ggcacgaat gccagaaaga actcccaact cccagccttt 500

ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550

cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600

aaatatcacc acaaaggag tatctgttag gagaaagaga caggtgtatg 650

gcaccgacag caggttcagc atcttgga aaaggttctt aaccaatttc 700

cctttcagca cagctgtgaa gctttccacg ggctgtagtgc gcatttcat 750

ttcccctcag catgttctaa ctgctgccca ctgtgttcat gatggaaagg 800

actatgtcaa agggagtaaa aagctaagg taggggtgtt gaagatgagg 850



cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350  
 atacattcta tgtatgaggt gctacatttt taggacaaag aattctgtaa 2400  
 tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450  
 tgaggactat agggatgaatt ctctgattag taattttaga tatgtccttt 2500  
 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296  
 <211> 413  
 <212> PRT  
 <213> Homo sapiens

<400> 296

Met	Glu	Asn	Met	Leu	Leu	Trp	Leu	Ile	Phe	Phe	Thr	Pro	Gly	Trp	1	5	10	15
Thr	Leu	Ile	Asp	Gly	Ser	Glu	Met	Glu	Trp	Asp	Phe	Met	Trp	His	20	25	30	
Leu	Arg	Lys	Val	Pro	Arg	Ile	Val	Ser	Glu	Arg	Thr	Phe	His	Leu	35	40	45	
Thr	Ser	Pro	Ala	Phe	Glu	Ala	Asp	Ala	Lys	Met	Met	Val	Asn	Thr	50	55	60	
Val	Cys	Gly	Ile	Glu	Cys	Gln	Lys	Glu	Leu	Pro	Thr	Pro	Ser	Leu	65	70	75	
Ser	Glu	Leu	Glu	Asp	Tyr	Leu	Ser	Tyr	Glu	Thr	Val	Phe	Glu	Asn	80	85	90	
Gly	Thr	Arg	Thr	Leu	Thr	Arg	Val	Lys	Val	Gln	Asp	Leu	Val	Leu	95	100	105	
Glu	Pro	Thr	Gln	Asn	Ile	Thr	Thr	Lys	Gly	Val	Ser	Val	Arg	Arg	110	115	120	
Lys	Arg	Gln	Val	Tyr	Gly	Thr	Asp	Ser	Arg	Phe	Ser	Ile	Leu	Asp	125	130	135	
Lys	Arg	Phe	Leu	Thr	Asn	Phe	Pro	Phe	Ser	Thr	Ala	Val	Lys	Leu	140	145	150	
Ser	Thr	Gly	Cys	Ser	Gly	Ile	Leu	Ile	Ser	Pro	Gln	His	Val	Leu	155	160	165	
Thr	Ala	Ala	His	Cys	Val	His	Asp	Gly	Lys	Asp	Tyr	Val	Lys	Gly	170	175	180	
Ser	Lys	Lys	Leu	Arg	Val	Gly	Leu	Leu	Lys	Met	Arg	Asn	Lys	Ser	185	190	195	
Gly	Gly	Lys	Lys	Arg	Arg	Gly	Ser	Lys	Arg	Ser	Arg	Arg	Glu	Ala	200	205	210	

Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu  
 215 220 225  
 Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln  
 230 235 240  
 Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys  
 245 250 255  
 Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp  
 260 265 270  
 Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala  
 275 280 285  
 His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys  
 290 295 300  
 Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp  
 305 310 315  
 Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu  
 320 325 330  
 Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser  
 335 340 345  
 Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys  
 350 355 360  
 Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp  
 365 370 375  
 Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg  
 380 385 390  
 Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Leu Trp Ile His Gly  
 395 400 405  
 Asn Asp Ala Asn Cys Ala Tyr Gly  
 410

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcatctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 298  
catcggtccc gtgaatccag aggc 24

<210> 299  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 299  
gaaggagggc cttcctttca gtggaccgg gtcaagaata cccac 45

<210> 300  
<211> 1869  
<212> DNA  
<213> Homo sapiens

<400> 300  
aatgtgagag gggctgatgg aagctgatag gcaggactgg agtggttagca 50  
ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100  
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150  
gcaactcctg gcacactgct cctctttctg gctttcctgc tcttgagttc 200  
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250  
gccccatggag tgaatgctca cgcacctgcg ggggaggggc ctctactct 300  
ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata 350  
cagaacatgc agtaatgtgg actgccacc agaagcaggt gatttccgag 400  
ctcagcaatg ctcagctcat aatgatgtca agcaccatgg ccagttttat 450  
gaatggcttc ctgtgtctaa tgaccctgac aacctatgtt cactcaagtg 500  
ccaagccaaa ggaacaaccc tggttgttga actagcacct aaggcttag 550  
atggtacgcy ttgctataca gaatctttgg atatgtgcat cagtgggtta 600  
tgccaaattg ttggctgcga tcaccagctg ggaagcaccg tcaaggaaga 650  
taactgtggg gtctgcaacg gagatgggtc cacctgccgg ctggtccgag 700  
ggcagtataa atcccagctc tccgcaacca aatcgatga tactgtggtt 750  
gcatttcct atggaagtag acatattcgc cttgtcttaa aaggctcctga 800  
tcatttatat ctggaaacca aaacctcca ggggactaaa ggtgaaaaca 850  
gtctcagctc cacaggaact ttccttgtgg acaattctag tgtggacttc 900

cagaaatttc	cagacaaaga	gatactgaga	atggctggac	cactcacagc	950
agatttcatt	gtcaagattc	gtaactcggg	ctccgctgac	agtacagtcc	1000
agttcatctt	ctatcaaccc	atcatccacc	gatggaggga	gacggatttc	1050
tttccttgct	cagcaacctg	tggaggaggt	tatcagctga	catcggctga	1100
gtgctacgat	ctgaggagca	accgtgtggt	tgctgaccaa	tactgtcact	1150
attaccaga	gaacatcaaa	cccaaacc	agcttcagga	gtgcaacttg	1200
gatccttgct	cagccagtga	cggatacaag	cagatcatgc	cttatgacct	1250
ctaccatccc	cttcctcggg	gggaggccac	cccatggacc	gcgtgctcct	1300
cctcgtgtgg	ggggggcatc	cagagccggg	cagtttcctg	tgtggaggag	1350
gacatccagg	ggcatgtcac	ttcagtggaa	gagtggaaat	gcgtgtacac	1400
ccctaagatg	cccacgcgc	agccctgcaa	catttttgac	tgccctaaat	1450
ggctggcaca	ggagtgggtc	ccgtgcacag	tgacatgtgg	ccagggcctc	1500
agataccgtg	tggctcctctg	catcgaccat	cgaggaatgc	acacaggagg	1550
ctgtagccca	aaaacaaagc	cccacataaa	agaggaatgc	atcgtaccca	1600
ctccctgcta	taaacccaaa	gagaaacttc	cagtcgaggc	caagttgcca	1650
tggttcaaac	aagctcaaga	gctagaagaa	ggagctgctg	tgtcagagga	1700
gccctcgtaa	gttgtaaaag	cacagactgt	tctatatattg	aaactgtttt	1750
gtttaaagaa	agcagtgtct	cactggttgt	agctttcatg	ggttctgaac	1800
taagtgtaat	catctcacca	aagctttttg	gctctcaa	taaagattga	1850
ttaqtttcaa	aaaaaaaaa	1869			

<210> 301

<211> 525

<212> PRT

<213> Homo sapiens

<400> 301

Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe  
1 5 10 15

Leu Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu  
20 25 30

Asp Arg Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys  
35 40 45

Ser Arg Thr Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys  
50 55 60



Leu Ser Ser Lys Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr  
 65 70 75  
 Cys Ser Asn Val Asp Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala  
 80 85 90  
 Gln Gln Cys Ser Ala His Asn Asp Val Lys His His Gly Gln Phe  
 95 100 105  
 Tyr Glu Trp Leu Pro Val Ser Asn Asp Pro Asp Asn Pro Cys Ser  
 110 115 120  
 Leu Lys Cys Gln Ala Lys Gly Thr Thr Leu Val Val Glu Leu Ala  
 125 130 135  
 Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp  
 140 145 150  
 Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln  
 155 160 165  
 Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly  
 170 175 180  
 Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln  
 185 190 195  
 Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr  
 200 205 210  
 Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu  
 215 220 225  
 Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser  
 230 235 240  
 Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp  
 245 250 255  
 Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro  
 260 265 270  
 Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala  
 275 280 285  
 Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg  
 290 295 300  
 Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly  
 305 310 315  
 Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn  
 320 325 330  
 Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile  
 335 340 345  
 Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro

350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met	Pro Tyr Asp Leu Tyr His	
365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro	Trp Thr Ala Cys Ser Ser	
380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg	Ala Val Ser Cys Val Glu	
395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser	Val Glu Glu Trp Lys Cys	
410	415	420
Met Tyr Thr Pro Lys Met Pro Ile Ala	Gln Pro Cys Asn Ile Phe	
425	430	435
Asp Cys Pro Lys Trp Leu Ala Gln Glu	Trp Ser Pro Cys Thr Val	
440	445	450
Thr Cys Gly Gln Gly Leu Arg Tyr Arg	Val Val Leu Cys Ile Asp	
455	460	465
His Arg Gly Met His Thr Gly Gly Cys	Ser Pro Lys Thr Lys Pro	
470	475	480
His Ile Lys Glu Glu Cys Ile Val Pro	Thr Pro Cys Tyr Lys Pro	
485	490	495
Lys Glu Lys Leu Pro Val Glu Ala Lys	Leu Pro Trp Phe Lys Gln	
500	505	510
Ala Gln Glu Leu Glu Glu Gly Ala Ala	Val Ser Glu Glu Pro Ser	
515	520	525

<210> 302  
 <211> 1533  
 <212> DNA  
 <213> Homo sapiens

<400> 302  
 cggacgcgtg ggcggcggct gcggaactcc cgtggagggg ccggtgggcc 50  
 ctcgggcctg acagatggca gtggccactg cggcggcagt actggccgct 100  
 ctgggcgggg cgctgtggct ggcgccccgc cgttcgtgg ggcccagggt 150  
 ccagcggctg cgcagaggcg gggaccccg cctcatgcac ggaagactg 200  
 tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgccgag 250  
 ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300  
 cgccgaggag gcggcgggtc agctccgccg cgagctccgc caggccgcgg 350  
 agtgcggccc agagcctggc gtcagcgggg tgggcgagct catagtccgg 400  
 gagctggacc tcgcctcgct gcgctcggtg cgcgccttct gccaggaaat 450

gctccaggaa gagcctaggc tggatgtctt gatcaataac gcagggatct 500  
 tccagtgcc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550  
 gtgaaccatc tggggcactt tctactcacc aatcttctcc ttggactcct 600  
 caaaagtcca gctcccagca ggattgtggt agtttcttcc aaactttata 650  
 aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700  
 aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750  
 ggaactagcc cgccgcttag aaggcacaaa tgtcacogtc aatgtgttgc 800  
 atcctggtat tgtacggaca aatctgggga ggcacataca cattccactg 850  
 ttggtcaaac cactcttcaa tttggtgtca tgggcttttt tcaaaactcc 900  
 agtagaaggt gccagactt ccatttattt ggctcttcca cctgaggtag 950  
 aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000  
 cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050  
 agtgatggtt ggctgctaa aataggaaca aggagtaaaa gagctgttta 1100  
 taaaactgca tatcagttat atctgtgatc aggaatggtg tggattgaga 1150  
 acttggtact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200  
 ggtacatgtg ggtatttttg agttactgaa aaattatttt tgggataaga 1250  
 gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300  
 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350  
 tggatgacat attaatat ttcagaatta agtgactcaa agtgctatcg 1400  
 agaggttttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450  
 ttactacaat gtttgggtgt tgtgtggaaa ttatctgcct ggtgtgtgca 1500  
 cacaagtctt acttgaata aatttactgg tac 1533

<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

Met Ala Val Ala Thr Ala Ala Ala Val Leu Ala Ala Leu Gly Gly  
 1 5 10 15

Ala Leu Trp Leu Ala Ala Arg Arg Phe Val Gly Pro Arg Val Gln  
 20 25 30

Arg Leu Arg Arg Gly Gly Asp Pro Gly Leu Met His Gly Lys Thr  
 35 40 45

Val Leu Ile Thr Gly Ala Asn Ser Gly Leu Gly Arg Ala Thr Ala  
50 55 60

Ala Glu Leu Leu Arg Leu Gly Ala Arg Val Ile Met Gly Cys Arg  
65 70 75

Asp Arg Ala Arg Ala Glu Glu Ala Ala Gly Gln Leu Arg Arg Glu  
80 85 90

Leu Arg Gln Ala Ala Glu Cys Gly Pro Glu Pro Gly Val Ser Gly  
95 100 105

Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg  
110 115 120

Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg  
125 130 135

Leu Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr  
140 145 150

Met Lys Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His  
155 160 165

Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys  
170 175 180

Ser Ser Ala Pro Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr  
185 190 195

Lys Tyr Gly Asp Ile Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser  
200 205 210

Tyr Asn Lys Ser Phe Cys Tyr Ser Arg Ser Lys Leu Ala Asn Ile  
215 220 225

Leu Phe Thr Arg Glu Leu Ala Arg Arg Leu Glu Gly Thr Asn Val  
230 235 240

Thr Val Asn Val Leu His Pro Gly Ile Val Arg Thr Asn Leu Gly  
245 250 255

Arg His Ile His Ile Pro Leu Leu Val Lys Pro Leu Phe Asn Leu  
260 265 270

Val Ser Trp Ala Phe Phe Lys Thr Pro Val Glu Gly Ala Gln Thr  
275 280 285

Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu Gly Val Ser Gly  
290 295 300

Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu Pro Lys Ala  
305 310 315

Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser Glu Val  
320 325 330

Met Val Gly Leu Leu Lys

<210> 304  
 <211> 521  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 20, 34, 62, 87, 221, 229  
 <223> unknown base

<400> 304  
 ggggattgta aagaggaagn actgtgccca aagntatgga tgaatctgtt 50  
 gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100  
 ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150  
 gtgatcagga atggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200  
 tttgatattg gaatagcctg ntaagaggna catgtgggta ttttgagatt 250  
 actgaaaaat tatttttggg ataagagaat ttcagcaaag atgtttttaa 300  
 tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350  
 attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400  
 gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450  
 tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500  
 tggaaattat ctgcctggct t 521

<210> 305  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 305  
 ccaggaaatg ctccaggaag agcc 24

<210> 306  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 306  
 gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 307  
aacgcaggga tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308  
<211> 1523  
<212> DNA  
<213> Homo sapiens

<400> 308  
gagaggacga ggtgccgtg cctggagaat cctccgtgc cgtcggtcc 50  
cggagcccag ccctttcta acccaacca acctagcca gtcccagccg 100  
ccagcgctg tccctgtcac ggacccagc gttaccatgc atcctgccgt 150  
cttcctatcc ttaccgacc tcagatgctc cttctgctc ctggtaactt 200  
gggtttttac tcctgtaaca actgaaataa caagtcttgc tacagagaat 250  
atagatgaaa ttttaacaa tgctgatgtt gctttagtaa atttttatgc 300  
tgactggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350  
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450  
caaatacca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550  
caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600  
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650  
cggacaacta tagagttttt gaacgagtag cgaatatttt gcatgatgac 700  
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750  
tggcgacaac ataactaca aaccaccagg gcattctgct ccggatatgg 800  
tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850  
gataaatgtg ttcctcttgt ccgagaaata acatttgaaa atggagagga 900  
attgacagaa gaaggactgc cttttctcat actctttcac atgaagaag 950  
atacagaaag tttagaata ttccagaatg aagtagctcg gcaattaata 1000  
agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050

acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100  
ctattgacag ctttaggcac atgtatgtgt ttggagactt caaagatgta 1150  
ttaattcctg gaaaactcaa gcaattcgta ttgacttac attctggaaa 1200  
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250  
gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300  
aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350  
gctttaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400  
cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450  
tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500  
aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309  
<211> 406  
<212> PRT  
<213> Homo sapiens

<400> 309  
Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser  
1 5 10 15  
Leu Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu  
20 25 30  
Ile Thr Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn  
35 40 45  
Ala Asp Val Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe  
50 55 60  
Ser Gln Met Leu His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile  
65 70 75  
Lys Glu Glu Phe Pro Asn Glu Asn Gln Val Val Phe Ala Arg Val  
80 85 90  
Asp Cys Asp Gln His Ser Asp Ile Ala Gln Arg Tyr Arg Ile Ser  
95 100 105  
Lys Tyr Pro Thr Leu Lys Leu Phe Arg Asn Gly Met Met Met Lys  
110 115 120  
Arg Glu Tyr Arg Gly Gln Arg Ser Val Lys Ala Leu Ala Asp Tyr  
125 130 135  
Ile Arg Gln Gln Lys Ser Asp Pro Ile Gln Glu Ile Arg Asp Leu  
140 145 150  
Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys Arg Asn Ile Ile Gly  
155 160 165

Tyr Phe Glu Gln Lys Asp Ser Asp Asn Tyr Arg Val Phe Glu Arg  
 170 175 180  
 Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu Ser Ala Phe  
 185 190 195  
 Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile  
 200 205 210  
 Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly  
 215 220 225  
 Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys  
 230 235 240  
 Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu  
 245 250 255  
 Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys  
 260 265 270  
 Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg  
 275 280 285  
 Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp  
 290 295 300  
 Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro  
 305 310 315  
 Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr  
 320 325 330  
 Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys  
 335 340 345  
 Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe  
 350 355 360  
 His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala  
 365 370 375  
 Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu  
 380 385 390  
 Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu  
 395 400 405

Leu

<210> 310  
 <211> 182  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure



<222> 36, 48  
<223> unknown base

<400> 310  
attaaggaag aatttccaaa tgaaaatcaa gtagtntttg ccagagtnga 50  
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100  
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150  
ggtcagcgat cagtgaagc attggcagat ta 182

<210> 311  
<211> 598  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396  
<223> unknown base

TECHNICAL FOOT  
<400> 311  
agaggcctct ctggaagttg tcccgggtgt tcgccgngg agcccgggtc 50  
gagaggacna ggtgccgtg cctggagaat cctccgctgc cgtcggctcc 100  
cggagcccag ccctttccta acccaacca acctagccn gtcccagccg 150  
ccagcgctg tccctgtcnc gganccagc gtnaccatgc atcctgccgt 200  
cttctatcc ttaccgacc tcagatgctc cttctgctc ctggtactt 250  
gggtttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300  
atagatgaaa ttttaacna tgctgatgtg gctttagtca atttttatgc 350  
tgactgggtg cgtttcagtc agatgtggca tccaattttt gaggangctt 400  
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500  
caaataccca accctcaat tgtttcgtaa tgggatgatg atgaagagag 550  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 312  
tgagaggcct ctctggaagt tg 22

<210> 313  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 313  
gtcagcgatc agtgaaagc 19

<210> 314  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 314  
ccagaatgaa gtagctcggc 20

<210> 315  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 315  
ccgactcaaa atgcattgtc 20

<210> 316  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 316  
catttggcag gaattgtcc 19

<210> 317  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 317  
ggtgctatag gccaaagg 18

<210> 318  
<211> 24  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgctttccta tccttaccg acctcagatg ctcccttctg ctctg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

gcccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50

cgctgctgct cactgccgcg ctcatcttct tcgccatttg gcacattata 100

gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

tacctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200

gtgtcatgtt tctttgtgca gcagagtggc ttactactggg tctcaatatg 250

cccctcttgg catatcatat ttggaggtat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaacat catgaatgca gatattctag 350

catattgtca gaaggaagga tggtgcaaat tagcttttta tcttctagca 400

tttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450

caacacacag aagaattggt ccagttaagt gcatgcaaaa agccaccaa 500

tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcotta ttttttaa at gtttccacat 600  
 ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650  
 taaatggtat tacgtataaa ttaatatata atgattacct ctggtgttga 700  
 caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750  
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800  
 cttgtagggc tcatttttgg ttcattgaaa cagtatctaa ttataaatta 850  
 gctgtagata tcaggtgctt ctgatgaagt gaaaatgtat atctgactag 900  
 tgggaaactt catgggtttc ctcactgtgc atgtcgatga ttatatatgg 950  
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000  
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050  
 taaatatact tgctttaatt ctttaagcata agtaaactg atataaaaat 1100  
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaatgtgt 1150  
 ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg 1200  
 ttctaactctg gtggttaaagg tattcttaag aatttgcagg tactacagat 1250  
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300  
 gtgcaatata ataaaactct gaaattaaga ctc 1333

<210> 322

<211> 144

<212> PRT

<213> Homo sapiens

<400> 322

Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu  
 1 5 10 15

Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala  
 20 25 30

Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys  
 35 40 45

Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala  
 50 55 60

Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu  
 65 70 75

Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met  
 80 85 90

Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr  
 95 100 105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp  
 110 115 120  
 Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr  
 125 130 135  
 Gly Met Ile Tyr Val Leu Val Ser Ser  
 140

<210> 323  
 <211> 477  
 <212> DNA  
 <213> Homo sapiens

<400> 323  
 attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50  
 tgtaataccc tgaatcccct tgtactcca gactaccca tccacgcttt 100  
 cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150  
 atatgccct cttggcatat catatttga ggtatatgag tagaccagt 200  
 atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250  
 tctagcatat tgcagaagg aaggatggtg caaattagct ttttatcttc 300  
 tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350  
 tagaacaaca cacagaagaa ttggtccagt taagtgcag caaaaagcca 400  
 ccaaataag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450  
 gaatctgac agttacttta aaaaatg 477

<210> 324  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 324  
 tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 325  
 caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326

<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 326  
gtgcagcaga gtggcttaca 20

<210> 327  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 327  
actggaccaa ttcttctgtg 20

<210> 328  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 328  
gatattctag catattgtca gaaggaagga tgggtgcaaat tagct 45

<210> 329  
<211> 1174  
<212> DNA  
<213> Homo sapiens

<400> 329  
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50  
tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100  
ggacccaact ggggctcccg ccgctgctgc tgctgaccat ggccttggcc 150  
ggaggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200  
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250  
accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300  
tcaatttgtc agtttgtgga tgatggaatt gacttaaata gaactaaatt 350  
ggaatgtgaa tctgcatgta cagaagcata ttccaatct gatgagcaat 400  
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450  
caagaacaac ttatgtocct gatgccaaaa atgcacctac tctttcctct 500

aactctggtg aggtcattct ggagtgcacat gatggactcc gcacagagct 550  
tcataacctc ttcattgact ttttatcttc aagccgatga cggaaaaata 600  
gttatattcc agtctaagcc agaaatccag tacgcaccac atttgagca 650  
ggagcctaca aatttgagag aatcatctct aagcaaaatg tcctatctgc 700  
aatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750  
gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800  
aactcttgct ctctcggtga tggattgct ttggatttgt tgtgcaactg 850  
ttgctacagc tgtggagcag tatgttcct ctgagaagct gagtatctat 900  
ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950  
ttctcttggtg gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000  
ctctacctac aaaagtgaat cttgctcatt ctgaaattta agcatttttc 1050  
ttttaaaaga caagtgaat agacatctaa aattccactc ctcatagagc 1100  
ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150  
caaataaagt tactcaaac tgtg 1174

<210> 330  
<211> 323  
<212> PRT  
<213> Homo sapiens

<400> 330  
Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly  
1 5 10 15  
Leu Pro Pro Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser  
20 25 30  
Gly Thr Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr  
35 40 45  
Ala Ser Cys His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr  
50 55 60  
Tyr Pro Lys Glu Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg  
65 70 75  
Leu Phe Ser Ile Cys Gln Phe Val Asp Asp Gly Ile Asp Leu Asn  
80 85 90  
Arg Thr Lys Leu Glu Cys Glu Ser Ala Cys Thr Glu Ala Tyr Ser  
95 100 105  
Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln  
110 115 120

Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met  
 125 130 135  
 Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe  
 140 145 150  
 Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser  
 155 160 165  
 Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile Phe  
 170 175 180  
 Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu  
 185 190 195  
 Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu  
 200 205 210  
 Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp Gly  
 215 220 225  
 Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp  
 230 235 240  
 Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp  
 245 250 255  
 Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro  
 260 265 270  
 Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu  
 275 280 285  
 Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg  
 290 295 300  
 Ser Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys  
 305 310 315  
 Val Asn Leu Ala His Ser Glu Ile  
 320

<210> 331  
 <211> 350  
 <212> DNA  
 <213> Homo sapiens

<400> 331  
 ttgggtgata cggcgtcttg ccaccgggcc tgtcagttga cctaccctt 50  
 gcacacctac cctaaggaag aggagttgta cgcattgtcag agaggttgca 100  
 ggctgttttc aattgtcag tttgtggatg atggaattga cttaaactga 150  
 actaaattgg aatgtgaatc tgcatgtaca gaagcatatt cccaatctga 200  
 tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250



aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300  
tttcctctaa ctctgggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332  
<211> 562  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 47  
<223> unknown base

<400> 332  
cacactggcc ggatctttta gagtcctttg accttgacca agggtcngga 50  
aaacagcaac aagctgagct gctgtgacag agggacaag atggcggcgc 100  
cgaagggagc ctttgggtga ggaaccaact ggggctcccg ccgctgctgc 150  
tgctgaccat ggccttgccg ggaggttcgg ggaccgcttc ggctgaagca 200  
tttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250  
gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300  
agagaggttg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350  
gacttaaadc gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400  
ttcccaatct gatgagcaat atgcttgcca tcttgggtgc cagaatcagc 450  
tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgcaaaa 500  
atgcacctac tcttctctct aactctgggtg aggtcattct ggagtacat 550  
gatggactcc gc 562

<210> 333  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 333  
acaagctgag ctgctgtgac ag 22

<210> 334  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 334  
tgattctggc aaccaagatg gc 22

<210> 335  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 335  
atggccttgg cgggaggttc ggggaccgct tcggctgaag 40

<210> 336  
<211> 1885  
<212> DNA  
<213> Homo sapiens

<400> 336  
gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50  
cgccccggag gtggggcgcc gctggggccg gcccgcacgg gcttcatctg 100  
agggcgcacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150  
gcgacaagct gccggagctg caatgggccc cggctgggga ttcttgttt 200  
gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250  
cccccgga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300  
ggatgattgt acctgtgatg ttgaaacat tgatagattt aataactaca 350  
ggcttttccc aagactacaa aaacttcttg aaagtacta ctttaggtat 400  
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450  
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500  
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550  
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600  
tctgagttag gaaacacaga aggctgttct tcagtggacc aagcatgatg 650  
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700  
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750  
accagatgct tggaaaaatat ggaatgtcat ctacgaagaa aactgtttta 800  
agccacagac aattaaaaga cttttaaatc ctttggttc tggtaaggg 850  
acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900  
aaaaagagca ttctacagac ttatatctgg octacatgca agcattaatg 950

tgcatttgag tgcaagatat cttttacaag agacctgggt agaaaagaaa 1000  
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050  
 tgaaggagaa ggtccaagaa ggcttaagaa cttgtatgtt ctctacttaa 1100  
 tagaactaag ggctttatcc aaagtgttac cattcttcga gcgccagat 1150  
 ttccaactct ttactggaaa taaaattcag gatgaggaaa acaaatgtt 1200  
 acttctggaa atacttcag aaatcaagtc atttccttg cattttgatg 1250  
 agaattcatt tttgtctgg gataaaaaag aagcacacaa actaaaggag 1300  
 gactttcgac tgcattttag aaatatttca agaattatgg attgtgttg 1350  
 ttgttttaaa tgcgtctgt ggggaaagct tcagactcag ggtttggca 1400  
 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450  
 agtggaccta gttatgaatt ccactaacc agacaagaaa tagtatcatt 1500  
 attcaacgca ttggaagaa tttctacaag tgtgaagaa ttagaaaact 1550  
 tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatattgac 1600  
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650  
 atagcaatga cagtcttaag ccaaacttt tatataaagt tgcttttga 1700  
 aaggagaatt atattgtttt aagtaaacc atttttaaaa attgtgttaa 1750  
 gtctatgtat aatactactg tgagtaaaag taatacttta ataattgtgt 1800  
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337  
 <211> 468  
 <212> PRT  
 <213> Homo sapiens

<400> 337  
 Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu Gly Ala Val  
 1 5 10 15  
 Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr  
 20 25 30  
 Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp  
 35 40 45  
 Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg  
 50 55 60  
 Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg  
 65 70 75

Tyr Tyr Lys Val Asn Leu Lys Arg Pro Cys Pro Phe Trp Asn Asp  
80 85 90

Ile Ser Gln Cys Gly Arg Arg Asp Cys Ala Val Lys Pro Cys Gln  
95 100 105

Ser Asp Glu Val Pro Asp Gly Ile Lys Ser Ala Ser Tyr Lys Tyr  
110 115 120

Ser Glu Glu Ala Asn Asn Leu Ile Glu Glu Cys Glu Gln Ala Glu  
125 130 135

Arg Leu Gly Ala Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys  
140 145 150

Ala Val Leu Gln Trp Thr Lys His Asp Asp Ser Ser Asp Asn Phe  
155 160 165

Cys Glu Ala Asp Asp Ile Gln Ser Pro Glu Ala Glu Tyr Val Asp  
170 175 180

Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp  
185 190 195

Ala Trp Lys Ile Trp Asn Val Ile Tyr Glu Glu Asn Cys Phe Lys  
200 205 210

Pro Gln Thr Ile Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly Gln  
215 220 225

Gly Thr Ser Glu Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu  
230 235 240

Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His  
245 250 255

Ala Ser Ile Asn Val His Leu Ser Ala Arg Tyr Leu Leu Gln Glu  
260 265 270

Thr Trp Leu Glu Lys Lys Trp Gly His Asn Ile Thr Glu Phe Gln  
275 280 285

Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro Arg Arg  
290 295 300

Leu Lys Asn Leu Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala Leu  
305 310 315

Ser Lys Val Leu Pro Phe Phe Glu Arg Pro Asp Phe Gln Leu Phe  
320 325 330

Thr Gly Asn Lys Ile Gln Asp Glu Glu Asn Lys Met Leu Leu Leu  
335 340 345

Glu Ile Leu His Glu Ile Lys Ser Phe Pro Leu His Phe Asp Glu  
350 355 360

Asn Ser Phe Phe Ala Gly Asp Lys Lys Glu Ala His Lys Leu Lys

	365		370		375
Glu Asp Phe Arg	Leu His Phe Arg Asn	Ile Ser Arg Ile Met Asp			
	380	385			390
Cys Val Gly Cys	Phe Lys Cys Arg Leu	Trp Gly Lys Leu Gln Thr			
	395	400			405
Gln Gly Leu Gly	Thr Ala Leu Lys Ile	Leu Phe Ser Glu Lys Leu			
	410	415			420
Ile Ala Asn Met	Pro Glu Ser Gly Pro	Ser Tyr Glu Phe His Leu			
	425	430			435
Thr Arg Gln Glu	Ile Val Ser Leu Phe	Asn Ala Phe Gly Arg Ile			
	440	445			450
Ser Thr Ser Val	Lys Glu Leu Glu Asn	Phe Arg Asn Leu Leu Gln			
	455	460			465
Asn Ile His					

<210> 338  
<211> 507  
<212> DNA  
<213> Homo sapiens

```
<220>  
<221> unsure  
<222> 101, 263, 376, 397, 426  
<223> unknown base
```

<400> 338  
gctggaaata tggatgtcat ctacgagaaa ctgttttaag ccacagacaa 50  
ttaaaagacc tttaaactct ttggcttctg gtcaagggac aagtgaagag 100  
nacacttttt acagttggct agaaggctct tgtgtagaaa aaagagcatt 150  
ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200  
caagatatct ttacaagag acctggttag aaaagaaatg gggacacaac 250  
attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300  
tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350  
ctttatccaa agtgttacca ttcttngagc gccagattt tcaactnttt 400  
actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaaat 450  
acttcatgaa atcaagtcatt ttcctttgca ttttgatgag aattcatttt 500  
tttgctg 507

<210> 339  
<211> 20

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 339  
aagctgccgg agctgcaatg 20

<210> 340  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 340  
ttgcttctta atcctgagcg c 21

<210> 341  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 341  
aaaggaggac ttctgactgc 20

<210> 342  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 342  
agagattcat ccaactgctcc aagtcg 26

<210> 343  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 343  
tgtccagaaa caggcacata tcagc 25

<210> 344  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 344  
agacagcggc acagaggtgc ttctgccagg ttagtggtta ctggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345  
cggcgcgctg ggcggacgcg tggcggacg cgtgggttg gagggggcag 50  
gatgggaggg aaagtgaaga aaacagaaaa ggagaggac agaggccaga 100  
ggactttctca tactggacag aaaccgatca ggcattgaac tccccttcgt 150  
cactcacctg ttcttgcccc tgggttctct gacaggtctc tgctccccct 200  
ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250  
gaatttgat acagtgtctt acaacatgtt gggggtggac agcgatgat 300  
gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350  
tttatcgctg cctgtaggg gggggccaca atgccccatg tgccaagggc 400  
cacttaggtg actaccaact gggaaattca tctcatctct ctgtgaatat 450  
gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500  
tgagctaagg agagggtggt ggcagtgtct ctgaaggctc ataaaagaaa 550  
aaagagaagt gtggttaagg aaaatggtct gtgtggaggg gtcaaggagt 600  
taaaaaccct agaaagcaaa aggtaggtaa tgtcaggag tagtcttcat 650  
gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700  
gtaactatct ccccatccc caggcctgtg cccctctctg gtctcgtgct 750  
tgtggcagct ctgtcttcag ttctgggata tgtgccctg tggtatgctt 800  
attcagcct cagggaagcc tggcaccac tgccaacgt gagccagagg 850  
aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900  
gggcaaagcg gtatgatgcc tggcaaaggg cctgcatggc tctctcatt 950  
gtacctaat gtgcttgcaa aagctccatg ttctctaaca gattcagact 1000  
cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050  
caagggtggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100  
catggtgaaa ctccatctct actaaaaaaa aaaaaatata aaaattagct 1150

gggtgcgcta gtgcatgcct gtaatctcat ctactcggga ggctaagaca 1200  
 ggagactctc acttcaaccc aggaggtgga ggttgcggtg agccaagatt 1250  
 gtgcctctgc actctagcgt ggggtgacaga gtaagcgaga ctccatctca 1300  
 aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350  
 gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400  
 gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450  
 agaagacccc catctctaaa taaatgtttt aaaaat 1486

<210> 346  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 346  
 Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe  
 1 5 10 15  
 Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro  
 20 25 30  
 Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val  
 35 40 45  
 Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala  
 50 55 60  
 Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg  
 65 70 75  
 Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His  
 80 85 90  
 Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn  
 95 100 105  
 Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly  
 110 115 120  
 Phe Met Val Ser

<210> 347  
 <211> 509  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 22  
 <223> unknown base

<400> 347



cacagttccc caccatcact cntcccatc cttccaactt tatttttagc 50  
 ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100  
 ggagagggac agaggccaga ggactttctca tactggacag aaaccgatca 150  
 ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttct 200  
 gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250  
 tcccagggcc accagaagct gaatttggat acagtgtctt acaacatggt 300  
 gggggtggac agcgatggat gctggtgggc gcccctggg atgggccttc 350  
 aggcgaccgg aggggggacg tttatcgctg ccctgtaggg gggggccaca 400  
 atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450  
 tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500  
 tggtgatgg 509

<210> 348  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic oligonucleotide probe  
 <400> 348  
 agggacagag gccagaggac ttc 23

<210> 349  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic oligonucleotide probe

<400> 349  
 caggtgcata ttcacagcag gatg 24

<210> 350  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 350  
 ggaactcccc ttcgtcactc acctgttctt gcccctgggtg ttcct 45

<210> 351  
 <211> 2056  
 <212> DNA

<213> Homo sapiens

<400> 351

aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50  
catctgggtt tgggcagaaa ggagggtgct tcggagcccg ccctttctga 100  
gcttcctggg cgggctctag aacaattcag gcttcgctgc gactcagacc 150  
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200  
gctttatattt ggaaagaaac aatgttctag gtcaaactga gtctaccaa 250  
tgcagacttt cacaatggtt ctagaagaaa tctggacaag tcttttcatg 300  
tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350  
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400  
tcttgatgtg gagcccagtg atcgcgctg gagaaacagt gtactattct 450  
gtcgaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500  
ccccagcagc tgggtgtcac tcaactgaagg tcttgagtgt gatgtcactg 550  
atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600  
ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650  
ctcaaccatc cttaccgcag ctgggatgga gatcaccaa gatggcttcc 700  
acctggttat tgagctggag gacctgggc cccagtttga gttccttgtg 750  
gcctactgga ggaggagcc tggtgccgag gaacatgtca aaatggtgag 800  
gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850  
actgtgtgaa ggccagaca ttcgtgaagg ccattgggag gtacagcgcc 900  
ttcagccaga cagaatgtgt ggaggtgcaa ggagaggcca tccccctggt 950  
actggccctg tttgcctttg ttggcttcat gctgatcctt gtggtcgtgc 1000  
cactgttcgt ctggaaaatg ggcgggtgc tccagtactc ctgttgcccc 1050  
gtggtggtcc tcccagacac cttgaaaata accaattcac cccagaagtt 1100  
aatcagctgc agaaggagg aggtggatgc ctgtgccacg gctgtgatgt 1150  
ctoctgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200  
caggatgaag cgagaacctg gtctgcatga catggaaacc atgaggggac 1250  
aagttgtgtt tctgttttcc gccacggaca agggatgaga gaagtaggaa 1300  
gagcctgttg tctacaagtc tagaagcaac catcagaggc aggttggttt 1350  
gtctaacaga aactgactg aggttaggg gatgtgacct ctagactggg 1400

ggctgccact tgetggctga gcaaccctgg gaaaagtgc ttcacccctt 1450  
 cggtcctaag ttttctcatc tgtaatgggg gaattaccta cacacctgct 1500  
 aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550  
 tacaccacgc acttgcaagg ctagagggaa actggtgaca ctctacagtc 1600  
 tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650  
 gatcaaggac tctacacact ggggtgcttg gagagcccac tttcccagaa 1700  
 taatccttga gagaaaagga atcatgggag caatggtgtt gagttcactt 1750  
 caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800  
 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850  
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc-1900  
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950  
 gtaacatgtg catgtttgtt gtgtctcttt tttctgttgg taaagtacag 2000  
 aattcagcaa ataaaaaggg ccaccctggc caaaagcggg aaaaaaaaaa 2050  
 aaaaaa 2056

<210> 352  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 352  
 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu  
 1 5 10 15  
 Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp  
 20 25 30  
 Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser  
 35 40 45  
 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro  
 50 55 60  
 Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu  
 65 70 75  
 Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser  
 80 85 90  
 Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala  
 95 100 105  
 Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln  
 110 115 120

Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser  
 125 130 135  
 Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe  
 140 145 150  
 His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe  
 155 160 165  
 Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val  
 170 175 180  
 Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met  
 185 190 195  
 Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys  
 200 205 210  
 Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu  
 215 220 225  
 Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe  
 230 235 240  
 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp  
 245 250 255  
 Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val  
 260 265 270  
 Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile  
 275 280 285  
 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met  
 290 295 300  
 Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser  
 305 310

<210> 353  
 <211> 864  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 654, 711, 748, 827  
 <223> unknown base

<400> 353  
 tctgtgat gcacatctgg gtttggcaaa aggaggttgc ttcgagccgc 50  
 cctttctagc ttcttgccg gctctagaac aattcaggct tcgctgcgac 100  
 tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150  
 agaatgcttt attttgaaa gaaacaatgt tctaggtcaa actgagtcta 200

ccaaatgcag actttcacia tggttctaga agaaatctgg acaagtcttt 250  
 tcatgtgggt tttctacgca ttgattccat gtttgctcac agatgaagtg 300  
 gccattctgc ctgccctca gaacctctct gtactctcaa ccaacatgaa 350  
 gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400  
 attctgtcga ataccagggg gactacgaga gcctgtacac gagccacatc 450  
 tggatcccca gcagctgggt ctcactcact gaaggtcctg agtgtgatgt 500  
 cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggccca 550  
 cattgggctc acagacctca gcctggagca tctgaagca tccctttaat 600  
 agaaactcaa ccatacttac ccgacctggg atggagatca ccaaagatgg 650  
 cttnacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700  
 ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750  
 gaaccccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800  
 tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850  
 ggcgctgggt tgat 864

T O P E  
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

- <210> 354
- <211> 23
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 354
- aggcttcgct gcgactagac ctc 23
- <210> 355
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 355
- ccaggtcggg taaggatggt tgag 24
- <210> 356
- <211> 50
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe

<400> 356  
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357

<211> 1670

<212> DNA

<213> Homo sapiens

<400> 357

cccacgcgtc cgcccacgcg tccgaggagc aagagagaag agagactgaa 50

acagggagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100

ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150

agaggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200

tggagacctg gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250

agaggaggtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300

gctgagagga gttaggaagat caggagctag agggagactg gagggttccg 350

ggaaaagagc agaggaaaga ggaaagacac agagagacgg gagagagaag 400

aagagtgggt ttgaagggcg gatctcagtc cctggctgct ttggcatttg 450

gggaactggg actccctgtg gggaggagag gaaagctgga agtcctggag 500

ggacagggtc ccagaaggag gggacagagg agctgagaga ggggggcagg 550

gcgttgggca ggggtccctc ggaggcctcc tggggatggg ggctgcagct 600

cgtctgagcg cccctcgagc gctggtactc tgggctgcac tgggggcagc 650

agctcacatc ggaccagcac ctgaccccgga ggactggtgg agctacaagg 700

ataatctoca gggaaacttc gtgccagggc ctccctttctg gggcctggtg 750

aatgcagcgt ggagtctgtg tgctgtgggg aagcggcaga gcccctgga 800

tgtggagctg aagaggggtc tttatgaccc ctttctgccc ccattaaggc 850

tcagcactgg aggagagaag ctccggggaa ccttgtacaa cacgggccga 900

catgtctcct tcctgcctgc accccgacct gtggtcaatg tgtctggagg 950

tcccctcctt tacagccacc gactcagtga actgcggtg ctgtttggag 1000

ctcgcgacgg agccggctcg gaacatcaga tcaaccacca gggtttctct 1050

gctgaggtgc agtcattca cttcaaccag gaactctacg ggaatttcag 1100

cgctgcctcc cgcgcccca atggcctggc cattctcagc ctctttgtca 1150

acgttgccag tacctctaac ccattcctca gtcgcctcct taaccgcgac 1200

accatcactc gcattctcta caagaatgat gcctactttc ttcaagacct 1250

gagcctggag ctctgttcc ctgaatcctt cggttcac acctatcagg 1300  
 gctctctcag caccgcgcc tgctccgaga ctgtcacctg gacctcatt 1350  
 gaccgggccc tcaatatcac ctcccttcag atgcactccc tgagactcct 1400  
 gagccagaat cctccatctc agatcttcca gagcctcagc ggtaacagcc 1450  
 ggccctgca gcccttgcc cacagggcac tgaggggcaa cagggacccc 1500  
 cggcaccgag agaggcgctg ccgaggcccc aactaccgcc tgcattgtga 1550  
 tgggtgtccc catggctgct gagactcccc ttcgaggatt gcaccgccc 1600  
 gtcctaagcc tccccacaag gcgaggggag ttaccctaa aacaaagcta 1650  
 ttaaaggagc agaatactta 1670

<210> 358  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 358  
 Met Gly Ala Ala Arg Leu Ser Ala Pro Arg Ala Leu Val Leu  
 1 5 10 15  
 Trp Ala Ala Leu Gly Ala Ala Ala His Ile Gly Pro Ala Pro Asp  
 20 25 30  
 Pro Glu Asp Trp Trp Ser Tyr Lys Asp Asn Leu Gln Gly Asn Phe  
 35 40 45  
 Val Pro Gly Pro Pro Phe Trp Gly Leu Val Asn Ala Ala Trp Ser  
 50 55 60  
 Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu  
 65 70 75  
 Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser  
 80 85 90  
 Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg  
 95 100 105  
 His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser  
 110 115 120  
 Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu  
 125 130 135  
 Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn  
 140 145 150  
 His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln  
 155 160 165  
 Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly

170	175	180
Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn		
185	190	195
Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile		
200	205	210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu		
215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser		
230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile		
245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg		
260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser		
275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg		
290	295	300
Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro		
305	310	315
Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg		
320	325	

FOHEDT = 4802001

<210> 359

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 359

tctgctgagg tgcagctcat tcac 24

<210> 360

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 360

gaggctctgg aagatctgag atgg 24

<210> 361

<211> 50

<212> DNA

<213> Artificial Sequence



<220>  
<223> Synthetic oligonucleotide probe

<400> 361  
gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362  
<211> 3038

<212> DNA

<213> Homo sapiens

<400> 362  
ggcgccctggt tctgcgcgta ctggtgttac ggagcaggag caagaggtcg 50  
ccgccagcct ccgccgccga gcctcggttcg tgtccccgcc cctcgctcct 100  
gcagctactg ctacaaaacg ctggggcgcc caccctggca gactaacgaa 150  
gcagctccct tcccaccca actgcaggtc taattttgga cgctttgcct 200  
gccatttctt ccaggttgag ggagccgcag aggcggaggc tcgcgtattc 250  
ctgcagtcag caccacgctc gcccccgac gctcggtgct caggeccctc 300  
gcgagcgggg ctctccgtct gcggtccctt gtgaaggctc tgggcggctg 350  
cagaggccgg ccgtccggtt tggctcacct ctcccaggaa acttcacact 400  
ggagagccaa aaggagtgga agagcctgtc ttggagattt tcctggggaa 450  
atcctgaggt cattcattat gaagtgtacc gcgcgggagt ggctcagagt 500  
aaccacagtg ctgttcattg ctagagcaat tccagccatg gtggttccca 550  
atgccacttt attggagaaa cttttggaaa aatacatgga tgaggatggt 600  
gagtgggtgga tagccaaaca acgagggaaa agggccatca cagacaatga 650  
catgcagagt attttggacc ttcataataa attacgaagt cagggtgtatc 700  
caacagcctc taatatggag tatatgacat gggatgtaga gctggaaaga 750  
tctgcagaat cctgggctga aagttgcttg tgggaacatg gacctgcaag 800  
cttgcttcca tcaattggac agaatttggg agcacactgg ggaagatata 850  
ggccccgcac gtttcatgta caatcggtgt atgatgaagt gaaagacttt 900  
agctacccat atgaacatga atgcaacca tattgtccat tcaggtgttc 950  
tgccctgta tgtacacatt atacacaggt cgtgtgggca actagtaaca 1000  
gaatcggttg tgccattaat ttgtgtcata acatgaacat ctgggggcag 1050  
atatggcca aagctgtcta cctggtgtgc aattactccc caaagggaaa 1100  
ctggtggggc catgccctt acaaacatgg gcggccctgt tctgcttgcc 1150

cacctagttt tggagggggc tgtagagaaa atctgtgcta caaagaagg 1200  
tcagacaggt attatcccc tcgagaagag gaaacaaatg aaatagaacg 1250  
acagcagtca caagtccatg acacccatgt ccggacaaga tcagatgata 1300  
gtagcagaaa tgaagtcata agcgcacagc aaatgtcca aattgtttct 1350  
tgtgaagtaa gattaagaga tcagtgcaaa ggaacaacct gcaataggta 1400  
cgaatgtcct gctggctgtt tggatagtaa agctaaagt attggcagt 1450  
tacattatga aatgcaatcc agcatctgta gagctgcaat tcattatggt 1500  
ataatagaca atgatggtgg ctgggtagat atcactagac aaggaagaaa 1550  
gcattatttc atcaagtcca atagaaatgg tattcaaaca attggcaaat 1600  
atcagtctgc taattccttc acagtctcta aagtaacagt tcaggctgtg 1650  
acttgtgaaa caactgtgga acagctctgt ccatttcata agcctgcttc 1700  
acattgcccc agagtatact gtcctcgtaa ctgtatgcaa gcaaattccac 1750  
attatgctcg tgtaattgga actcgagttt attctgatct gtccagtatc 1800  
tgcagagcag cagtacatgc tggagtgggt cgaaatcacg gtggttatgt 1850  
tgatgtaatg cctgtggaca aaagaaagac ctacattgct tcttttcaga 1900  
atggaatcct ctcagaaagt ttacagaatc ctccaggagg aaaggcattc 1950  
agagtgtttg ctgttggtg aaactgaata cttggaagag gaccataaag 2000  
actattccaa atgcaatatt tctgaatttt gtataaaact gtaacattac 2050  
tgtacagagt acatcaacta ttttcagccc aaaaagggtgc caaatgcata 2100  
taaatcttga taaacaaagt ctataaaata aaacatggga cattagcttt 2150  
gggaaaagta atgaaaatat aatggtttta gaaatcctgt gttaaattatt 2200  
gctatatatt cttagcagtt atttctacag ttaattacat agtcatgatt 2250  
gttctacggt tcatatatta tatggtgctt tgtatatgcc actaataaaa 2300  
tgaatctaaa cattgaatgt gaatggccct cagaaaatca tctagtgcatt 2350  
ttaaaaataa tcgactctaa aactgaaaga aaccttatca cattttcccc 2400  
agttcaatgc tatgccatta ccaactccaa ataattctaa ataattttcc 2450  
acttaataac tgtaaagttt ttttctgtta atttaggcatt atagaatatt 2500  
aaattctgat attgcacttc ttattttata taaaataatc cttaaatatc 2550  
caaatgaatc tgttaaaatg tttgattcct tgggaatggc cttaaaaata 2600

aatgtaataa agtcagagtg gtggtatgaa aacattccta gtgatcatgt 2650  
 agtaaagtga gggtaagca tggacagcca gagctttcta tgtactgtta 2700  
 aaattgaggt cacatatattt cttttgtatc ctggcaaata ctctgcagg 2750  
 ccaggaagta taatagcaaa aagttgaaca aagatgaact aatgtattac 2800  
 attaccattg ccactgattt tttttaaatg gtaaatgacc ttgtatataa 2850  
 atattgccat atcatggtag ctataatggg gatataattg tttctatgaa 2900  
 aatgtattg tgctttgata ctaaaaatct gtaaaatggt agttttggta 2950  
 attttttttc tgctgggtgga tttacatatt aaattttttc tgctgggtgga 3000  
 taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

<210> 363  
 <211> 500  
 <212> PRT  
 <213> Homo sapiens

<400> 363  
 Met Lys Cys Thr Ala Arg Glu Trp Leu Arg Val Thr Thr Val Leu 15  
 1 5 10  
 Phe Met Ala Arg Ala Ile Pro Ala Met Val Val Pro Asn Ala Thr 30  
 20 25  
 Leu Leu Glu Lys Leu Leu Glu Lys Tyr Met Asp Glu Asp Gly Glu 45  
 35 40  
 Trp Trp Ile Ala Lys Gln Arg Gly Lys Arg Ala Ile Thr Asp Asn 60  
 50 55  
 Asp Met Gln Ser Ile Leu Asp Leu His Asn Lys Leu Arg Ser Gln 75  
 65 70  
 Val Tyr Pro Thr Ala Ser Asn Met Glu Tyr Met Thr Trp Asp Val 90  
 80 85  
 Glu Leu Glu Arg Ser Ala Glu Ser Trp Ala Glu Ser Cys Leu Trp 105  
 95 100  
 Glu His Gly Pro Ala Ser Leu Leu Pro Ser Ile Gly Gln Asn Leu 120  
 110 115  
 Gly Ala His Trp Gly Arg Tyr Arg Pro Pro Thr Phe His Val Gln 135  
 125 130  
 Ser Trp Tyr Asp Glu Val Lys Asp Phe Ser Tyr Pro Tyr Glu His 150  
 140 145  
 Glu Cys Asn Pro Tyr Cys Pro Phe Arg Cys Ser Gly Pro Val Cys 165  
 155 160  
 Thr His Tyr Thr Gln Val Val Trp Ala Thr Ser Asn Arg Ile Gly

170	175	180
Cys Ala Ile Asn Leu Cys His Asn Met	Asn Ile Trp Gly Gln Ile	
185	190	195
Trp Pro Lys Ala Val Tyr Leu Val Cys	Asn Tyr Ser Pro Lys Gly	
200	205	210
Asn Trp Trp Gly His Ala Pro Tyr Lys	His Gly Arg Pro Cys Ser	
215	220	225
Ala Cys Pro Pro Ser Phe Gly Gly Gly	Cys Arg Glu Asn Leu Cys	
230	235	240
Tyr Lys Glu Gly Ser Asp Arg Tyr Tyr	Pro Pro Arg Glu Glu Glu	
245	250	255
Thr Asn Glu Ile Glu Arg Gln Gln Ser	Gln Val His Asp Thr His	
260	265	270
Val Arg Thr Arg Ser Asp Asp Ser Ser	Arg Asn Glu Val Ile Ser	
275	280	285
Ala Gln Gln Met Ser Gln Ile Val Ser	Cys Glu Val Arg Leu Arg	
290	295	300
Asp Gln Cys Lys Gly Thr Thr Cys Asn	Arg Tyr Glu Cys Pro Ala	
305	310	315
Gly Cys Leu Asp Ser Lys Ala Lys Val	Ile Gly Ser Val His Tyr	
320	325	330
Glu Met Gln Ser Ser Ile Cys Arg Ala	Ala Ile His Tyr Gly Ile	
335	340	345
Ile Asp Asn Asp Gly Gly Trp Val Asp	Ile Thr Arg Gln Gly Arg	
350	355	360
Lys His Tyr Phe Ile Lys Ser Asn Arg	Asn Gly Ile Gln Thr Ile	
365	370	375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe	Thr Val Ser Lys Val Thr	
380	385	390
Val Gln Ala Val Thr Cys Glu Thr Thr	Val Glu Gln Leu Cys Pro	
395	400	405
Phe His Lys Pro Ala Ser His Cys Pro	Arg Val Tyr Cys Pro Arg	
410	415	420
Asn Cys Met Gln Ala Asn Pro His Tyr	Ala Arg Val Ile Gly Thr	
425	430	435
Arg Val Tyr Ser Asp Leu Ser Ser Ile	Cys Arg Ala Ala Val His	
440	445	450
Ala Gly Val Val Arg Asn His Gly Gly	Tyr Val Asp Val Met Pro	
455	460	465

Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile  
470 475 480

Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg  
485 490 495

Val Phe Ala Val Val  
500

<210> 364  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 364  
ggacagaatt tgggagcaca ctgg 24

<210> 365  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 365  
ccaagagtat actgtcctcg 20

<210> 366  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 366  
agcacagatt ttctctacag ccccc 25

<210> 367  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 367  
aaccactcca gcatgtactg ctgc 24

<210> 368  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369

<211> 1685

<212> DNA

<213> Homo sapiens

<400> 369

gcggagacaa gcgcagagcg cagcgcacgg ccacagacag ccctgggcat 50

ccaccgacgg cgcagccgga gccagcagag ccggaaggcg cgccccgggc 100

agagaaagcc gagcagagct ggggtggcgtc tccgggcccgc cgctccgacg 150

ggccagcgcc ctcccatgt ccctgctccc acgcccgcgc cctecgggtca 200

gcatgaggct cctggcggcc gcgctgctcc tgctgctgct ggcgctgtac 250

accgcgcgtg tggacgggtc caaatgcaag tgctcccga agggacccaa 300

gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccgcg 350

actgcgagga gaagatggtt atcatcacca ccaagagcgt gtccaggtag 400

cgaggtcagg agcactgcct gcaccccaag ctgcagagca ccaagcgctt 450

catcaagtgg tacaacgcct ggaacgagaa gcgcagggtc tacgaagaat 500

agggtgaaaa acctcagaag ggaaaaactcc aaaccagttg ggagacttgt 550

gcaaaggact ttgcagatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600

aaaaaaaaaa aaagcctttc tttctcacag gcataagaca caaattatat 650

attgttatga agcacttttt accaacggtc agtttttaca ttttatagct 700

gcgtgcgaaa ggcttccaga tgggagaccc atctctcttg tgctccagac 750

ttcatcacag gctgcttttt atcaaaaagg ggaaaactca tgcctttcct 800

ttttaaaaaa tgcttttttg tatttgtcca tacgtcacta tacatctgag 850

ctttataagc gcccgggagg aacaatgagc ttggtggaca catttcattg 900

cagtgttgct ccattcctag cttgggaagc ttccgcttag aggtcctggc 950

gcctcggcac agctgccacg ggctctcctg ggcttatggc cggtcacagc 1000

ctcagtgtga ctccacagtg gccctgtag ccgggcaagc aggagcaggt 1050

ctctctgcat ctgttctctg aggaactcaa gtttggttgc cagaaaaatg 1100

tgcttcattc cccctggtt aatttttaca caccctagga aacatttcca 1150

ccctgggcat

agatcctgtg atggcgagac aaatgatcct taaagaaggt gtggggtcct 1200  
 tcccaacctg aggatttctg aaaggttcac aggttcaata tttaatgctt 1250  
 cagaagcatg tgaggttccc aacactgtca gcaaaaacct taggagaaaa 1300  
 cttaaaaata tatgaatata tgcgcaatac acagctacag acacacattc 1350  
 tgttgacaag ggaaaacctt caaagcatgt ttctttccct caccacaaca 1400  
 gaacatgcag tactaaagca atatatttgt gattcccat gtaattcttc 1450  
 aatgttaaac agtgcagtcc tctttcgaaa gctaagatga ccatgcgccc 1500  
 tttcctctgt acatataccc ttaagaacgc cccctccaca cactgcccc 1550  
 cagtatatgc cgcattgtac tgctgtgta tatgctatgt acatgtcaga 1600  
 aaccattagc attgcatgca ggtttcatat tctttctaag atggaaagta 1650  
 ataaaatata tttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370

<211> 111

<212> PRT

<213> Homo sapiens

<400> 370

Met	Ser	Leu	Leu	Pro	Arg	Arg	Ala	Pro	Pro	Val	Ser	Met	Arg	Leu
1				5				10						15
Leu	Ala	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Ala	
				20				25						30
Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys
				35				40						45
Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr
				50				55						60
Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val
				65				70						75
Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln
				80				85						90
Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys
				95				100						105
Arg	Arg	Val	Tyr	Glu	Glu									
				110										

<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

cagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg ttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373

ctccggtcag catgaggctc ctggcgccg ctgctcctgc tgctg 45

<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

gccccaggga ctgctatggc ttcctttgtt gttcaccccg gtctgcgtca 50

tgtaaactc caatgtctc ctgtggttaa ctgctcttgc catcaagttc 100

accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150

caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200

tggagcagta cttaggggtc ccctatgcct cccccccac tggagagagg 250

cggtttcagc cccagaacc cccgtcctcc tggactggca tccgaaatac 300

tactcagttt gctgctgtgt gccccagca cctggatgag agatccttac 350

tgcatgacat gctgccatc tggtttaccg ccaatttga tactttgatg 400

acctatgttc aagatcaaaa tgaagactgc cttacttaa acatctacgt 450

gcccacggaa gatggagcca acacaaagaa aaacgcagat gatataacga 500

gtaatgaccg tggatgaagac gaagatatc atgatcagaa cagtaagaag 550

cccgtcatgg totatatcca tgggggatct tacatggagg gcaccggcaa 600

catgattgac ggcagcattt tggcaagcta cggaacgctc atcgtgatca 650



ccattaacta ccgctctgga atactagggt ttttaagtac cggtgaccag 700  
gcagcaaaaag gcaactatgg gctcctggat cagattcaag cactgcggtg 750  
gattgaggag aatgtgggag cctttggcgg ggacccaag agagtgacca 800  
tctttggctc gggggctggg gcctcctgtg tcagcctggt gaccctgtcc 850  
cactactcag aaggtctctt ccagaaggcc atcattcaga gcggcaccgc 900  
cctgtccagc tgggcagtga actaccagcc ggccaagtac actcggatat 950  
tggcagacaa ggtcggctgc aacatgctgg acaccacgga catggtagaa 1000  
tgcctgcgga acaagaacta caaggagctc atccagcaga ccatcacccc 1050  
ggccacctac cacatagcct tcggggccgt gatcgacggc gacgtcatcc 1100  
cagacgaccc ccagatcctg atggagcaag gcgagttcct caactacgac 1150  
atcatgctgg gcgtcaacca aggggaaggc ctgaagttcg tggacggcat 1200  
cgtggataac gaggacggtg tgacgcccaa cgactttgac ttctccgtgt 1250  
ccaacttcgt ggacaacctt tacggctacc ctgaaggga agacactttg 1300  
cgggagacta tcaagttcat gtacacagac tgggccgata aggaaaacc 1350  
ggagacgcgg cggaacc 1400  
tggccccgc cgtggccgc gacctgcacg cgcagtacgg ctccccacc 1450  
tacttctatg ccttctatca tctactgcaa agcgaaatga agcccagctg 1500  
ggcagattcg gccatggtg atgaggtccc ctatgtcttc ggcatccca 1550  
tgatcgggcc caccagctc ttcagttgta acttttcaa gaacgacgtc 1600  
atgctcagcg ccgtggtcat gacctactgg acgaacttcg ccaaaactgg 1650  
tgatccaaat caaccagttc ctcaggatac caagttcatt cacacaaaac 1700  
ccaaccgctt tgaagaagtg gcctggtcca agtataatcc caaagaccag 1750  
ctctatctgc atattggctt gaaaccaga gtgagagatc actaccgggc 1800  
aacgaaagtg gctttctggt tggaactcgt tctctatttg cacaacttga 1850  
acgagatatt ccagtatgtt tcaacaacca caaaggttcc tccaccagac 1900  
atgacatcat ttccctatgg caccggcgga tctcccgcca agatatggcc 1950  
aaccacaaa cgccagcaa tcaactctgc caacaatccc aaactctta 2000  
aggaccctca caaacaggg cctgaggaca caactgtcct cattgaaacc 2050  
aaacgagatt attccaccga attaatgtgc accattgccg tcggggcgctc 2100



Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro	50	55	60
				65					70					75			
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val			
				80					85					90			
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu			
				95					100					105			
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val			
				110					115					120			
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro			
				125					130					135			
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr			
				140					145					150			
Ser	Asn	Asp	Arg	Gly	Glu	Asp	Glu	Asp	Ile	His	Asp	Gln	Asn	Ser			
				155					160					165			
Lys	Lys	Pro	Val	Met	Val	Tyr	Ile	His	Gly	Gly	Ser	Tyr	Met	Glu			
				170					175					180			
Gly	Thr	Gly	Asn	Met	Ile	Asp	Gly	Ser	Ile	Leu	Ala	Ser	Tyr	Gly			
				185					190					195			
Asn	Val	Ile	Val	Ile	Thr	Ile	Asn	Tyr	Arg	Leu	Gly	Ile	Leu	Gly			
				200					205					210			
Phe	Leu	Ser	Thr	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu			
				215					220					225			
Leu	Asp	Gln	Ile	Gln	Ala	Leu	Arg	Trp	Ile	Glu	Glu	Asn	Val	Gly			
				230					235					240			
Ala	Phe	Gly	Gly	Asp	Pro	Lys	Arg	Val	Thr	Ile	Phe	Gly	Ser	Gly			
				245					250					255			
Ala	Gly	Ala	Ser	Cys	Val	Ser	Leu	Leu	Thr	Leu	Ser	His	Tyr	Ser			
				260					265					270			
Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	Ile	Gln	Ser	Gly	Thr	Ala	Leu			
				275					280					285			
Ser	Ser	Trp	Ala	Val	Asn	Tyr	Gln	Pro	Ala	Lys	Tyr	Thr	Arg	Ile			
				290					295					300			
Leu	Ala	Asp	Lys	Val	Gly	Cys	Asn	Met	Leu	Asp	Thr	Thr	Asp	Met			
				305					310					315			
Val	Glu	Cys	Leu	Arg	Asn	Lys	Asn	Tyr	Lys	Glu	Leu	Ile	Gln	Gln			
				320					325					330			
Thr	Ile	Thr	Pro	Ala	Thr	Tyr	His	Ile	Ala	Phe	Gly	Pro	Val	Ile			
				335					340					345			



635	640	645
Asn Pro Lys His Ser Lys Asp Pro His	Lys Thr Gly Pro Glu Asp	
650	655	660
Thr Thr Val Leu Ile Glu Thr Lys Arg	Asp Tyr Ser Thr Glu Leu	
665	670	675
Ser Val Thr Ile Ala Val Gly Ala Ser	Leu Leu Phe Leu Asn Ile	
680	685	690
Leu Ala Phe Ala Ala Leu Tyr Tyr Lys	Lys Asp Lys Arg Arg His	
695	700	705
Glu Thr His Arg Arg Pro Ser Pro Gln	Arg Asn Thr Thr Asn Asp	
710	715	720
Ile Ala His Ile Gln Asn Glu Glu Ile	Met Ser Leu Gln Met Lys	
725	730	735
Gln Leu Glu His Asp His Glu Cys Glu	Ser Leu Gln Ala His Asp	
740	745	750
Thr Leu Arg Leu Thr Cys Pro Pro Asp	Tyr Thr Leu Thr Leu Arg	
755	760	765
Arg Ser Pro Asp Asp Ile Pro Leu Met	Thr Pro Asn Thr Ile Thr	
770	775	780
Met Ile Pro Asn Thr Leu Thr Gly Met	Gln Pro Leu His Thr Phe	
785	790	795
Asn Thr Phe Ser Gly Gly Gln Asn Ser	Thr Asn Leu Pro His Gly	
800	805	810
His Ser Thr Thr Arg Val		
815		

704207 73027007

<210> 376  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 376  
 ggcaagctac ggaaacgtca tcgtg 25  
  
 <210> 377  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

gggaaagatg gcggcgactc tgggaccct tgggtcgtgg cagcagtggc 50

ggcgtatgtt gtcggctcgg gatgggtcca ggatgttact ctttcttctt 100

ttgttggggt ctgggcaggg gccacagcaa gtcggggcgg gtcaaacgtt 150

cgagtacttg aaacgggagc actcgtctgc gaagccctac caggggtgtgg 200

gcacaggcag ttcctcactg tggaatctga tgggcaatgc catggtgatg 250

accagtata tccgccttac ccagatatg caaagtaaac aggggtgcctt 300

gtggaaccgg gtgccatgtt tctgagaga ctgggagttg caggtgcact 350

tcaaatcca tggacaagga aagaagaatc tgcattggga tggcttgga 400

atctggtaca caaaggatcg gatgcagcca gggcctgtgt ttggaacat 450

ggacaaattt gtggggctgg gagtatttgt agacacctac cccaatgagg 500

agaagcagca agagcgggta ttccctaca tctcagccat ggtgaacaac 550

ggctccctca gctatgatca tgagcgggat gggcggccta cagagctggg 600

aggctgcaca gccattgtcc gcaatcttca ttacgacacc ttcttggtga 650

ttcgctacgt caagaggcat ttgacgataa tgatggatat tgatggcaag 700

catgagtga gggactgcat tgaagtgcc ggagtccgcc tgccccgcgg 750

ctactacttc ggcacctcct ccatcactgg ggatctctca gataatcatg 800

atgtcatttc cttgaagttg tttgaactga cagtggagag aaccccagaa 850

gaggaaaagc tccatcgaga tgtgttcttg ccctcagtgg acaatatgaa 900

gctgcctgag atgacagctc cactgccgcc cctgagtggc ctggccctct 950

tcctcatcgt cttttctcc ctggtgtttt ctgtatttgc catagtcatt 1000

TCAGTACTTG

ggtatcatac tctacaacaa atggcaggaa cagagccgaa agcgcttcta 1050  
 ctgagccctc ctgctgccac cacttttgtg actgtcaccc atgaggtatg 1100  
 gaaggagcag gcactggcct gagcatgcag cctggagagt gttcttgtct 1150  
 ctagcagctg gttggggact atattctgtc actggagttt tgaatgcagg 1200  
 gaccccgcat tcccatgggt gtgcatgggg acatctaact ctggctctggg 1250  
 aagccaccca cccaggga atgctgctgt gatgtgcctt tccctgcagt 1300  
 ccttccatgt gggagcagag gtgtgaagag aatttacgtg gttgtgatgc 1350  
 caaaatcaca gaacagaatt tcatagccca ggctgccgtg ttgtttgact 1400  
 cagaaggccc ttctacttca gttttgaatc cacaaagaat taaaaactgg 1450  
 taacaccaca ggctttctga ccatccattc gttgggtttt gcatttgacc 1500  
 caacctctg cctacctgag gagctttctt tggaaaccag gatggaaact 1550  
 tcttccctgc cttaccttc tttactcca ttcattgtcc tctctgtgtg 1600  
 caacctgagc tgggaaaggc atttggatgc ctctctgttg gggcctgggg 1650  
 ctgcagaaca cacctgcgtt tcaactggcct tcattaggtg gccctaggga 1700  
 gatggcttct tgctttggat cactgttccc tagcatgggt cttgggtcta 1750  
 ttggcatgtc catggccttc ccaatcaagt ctcttcaggc cctcagtga 1800  
 gtttggttaa aggttgggtg aaaaatcaag agaagcctg aagacatcat 1850  
 ggatgccatg gattagctgt gcaactgacc agctccaggt ttgatcaaac 1900  
 caaaagcaac atttgtcatg tggctgacc atgtggagat gtttctggac 1950  
 ttgctagagc ctgcttagct gcatgttttg tagttacgat ttttggaatc 2000  
 ccactttgag tgctgaaagt gtaaggaagc tttcttctta caccttgggc 2050  
 ttggatattg cccagagaag aaatttggt tttttttct taatggacaa 2100  
 gagacagttg ctgttctcat gttccaagtc tgagagcaac agaccctcat 2150  
 catctgtgcc tggaagagtt cactgtcatt gagcagcaca gcctgagtgc 2200  
 tggcctctgt caacccttat tccactgcct tatttgacaa ggggttacat 2250  
 gctgctcacc ttactgcctt gggattaaat cagttacagg ccagagtctc 2300  
 cttggagggc ctggaactct gactcctcct atgaacctct gtagcctaaa 2350  
 tgaaattctt aaaatcaccg atggaaccaa aaaaaaaaaa aaaaaggcg 2400  
 gccgcgactc tagagtcgac ctgcagtagg gataacaggg taataagctt 2450

ggccgccatg g 2461

<210> 380

<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

Met	Ala	Ala	Thr	Leu	Gly	Pro	Leu	Gly	Ser	Trp	Gln	Gln	Trp	Arg
1				5					10					15
Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly
				35					40					45
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro
				50					55					60
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met
				65					70					75
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp
				80					85					90
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe
				95					100					105
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln
				110					115					120
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr
				125					130					135
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys
				140					145					150
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu
				155					160					165
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn
				170					175					180
Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr
				185					190					195
Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp
				200					205					210
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met
				215					220					225
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val
				230					235					240
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser
				245					250					255



Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys  
260 265 270

Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu  
275 280 285

His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro  
290 295 300

Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe  
305 310 315

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val  
320 325 330

Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys  
335 340 345

Arg Phe Tyr

1000  
900  
800  
700  
600  
500  
400  
300  
200  
100  
0

<210> 381  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 381  
ccttgggtcg tggcagcagt gg 22

<210> 382  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 382  
cactctccag gctgcatgct cagg 24

<210> 383  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 383  
gtcaaactgt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384  
<211> 3150  
<212> DNA  
<213> Homo sapiens

<400> 384

ccgagccggg cgcgagcga cgagctggg gccggcctgg gaccatgggc 50  
gtgagtcaa tctacggatc agtctctgat ggtgggtcgt taacctcagt 100  
ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150  
tggggctctgg ctgagaattc ctgcagctgg tgaaaatctg ttttctagaa 200  
gagggtttaat taatgcctgc agtctgacat gttcccgatt tgaggtgaaa 250  
ccatgaagag aaaatagaat acttaataat gcttttccgc aaccgcttct 300  
tgctgctgct ggccctggct gcgctgctgg cctttgtgag cctcagcctg 350  
cagttcttcc acctgatccc ggtgtcgact cctaagaatg gaatgagtag 400  
caagagtcca aagagaatca tgcccgaccc tgtgacggag cccctgtga 450  
cagaccccg tttatgaagct cttttgtact gcaacatccc cagtgtggcc 500  
gagcgagca tggaaggtca tgcccgcac cattttaagc tggctcagt 550  
gcatgtgttc attcgccacg gagacaggta cccactgtat gtcattccca 600  
aaacaaagcg accagaaatt gactgcactc tgggtggctaa caggaaaccg 650  
tatcaccxaa aactggaagc tttcattagt cacatgtcaa aaggatccg 700  
agcctcttcc gaaagccct tgaactcctt gcctctttac ccaaaccacc 750  
cattgtgtga gatgggagag ctcacacaga caggagtgtg gcagcatttg 800  
cagaacggc agctgctgag ggatatctat ctaaagaaac acaaaactcct 850  
gcccaatgat tggctctgcag accagctcta tttagagacc actgggaaaa 900  
gccggaccct acaaagtggg ctggccttgc tttatggctt tctcccagat 950  
tttgactgga agaagattta tttcaggcac cagccaagtg cgctgttctg 1000  
ctctggaagc tgctattgcc cgtaagaaa ccagtatctg gaaaaggagc 1050  
agcgtcgtca gtacctcta cgtttgaaaa acagccagct ggagaagacc 1100  
tacggggaga tggccaagat cgtggatgtc cccaccaagc agcttagagc 1150  
tgccaacccc atagactcca tgctctgcca cttctgccac aatgtcagct 1200  
ttccctgtac cagaaatggc tgtgttgaca tggagcactt caaggtaatt 1250  
aagaccatc agatcgagga tgaaagggaa agacgggaga agaaattgta 1300  
cttcgggtat tctctcctgg gtgcccaccc catctgaac caaacatcg 1350  
gccgatgca gcgtgccacc gagggcagga aagaagagct ctttgccctc 1400  
tactctgctc atgatgtcac tctgtcacca gttctcagt ccttgggcct 1450



attgattttt aaatgcgttt ttggaagaac tttgctatta ggtagtttac 2950  
 agatctttat aagggtgtttt atatattaga agcaattata attacatctg 3000  
 tgatttctga actaatggtg ctaattcaga gaaatggaaa gtgaaagtga 3050  
 gattctctgt tgtcatcggc attccaactt tttctctttg tttttgtcca 3100  
 gtgttgcat tgaatatgtc tgtttctata aataaatttt ttaagaataa 3150

<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

Met	Leu	Phe	Arg	Asn	Arg	Phe	Leu	Leu	Leu	Leu	Ala	Leu	Ala	Ala	1	5	10	15
Leu	Leu	Ala	Phe	Val	Ser	Leu	Ser	Leu	Gln	Phe	Phe	His	Leu	Ile	20	25	30	
Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys	35	40	45	
Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro	50	55	60	
Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu	65	70	75	
Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser	80	85	90	
Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val	95	100	105	
Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala	110	115	120	
Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His	125	130	135	
Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Glu	Ser	Pro	Leu	Asn	Ser	140	145	150	
Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Glu	Met	Gly	Glu	Leu	155	160	165	
Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu	170	175	180	
Arg	Asp	Ile	Tyr	Leu	Lys	Lys	His	Lys	Leu	Leu	Pro	Asn	Asp	Trp	185	190	195	
Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr	200	205	210	

Protein Data Bank

Leu Gln Ser Gly	Leu Ala Leu Leu Tyr	Gly Phe Leu Pro Asp	Phe
215		220	225
Asp Trp Lys Lys	Ile Tyr Phe Arg His	Gln Pro Ser Ala Leu	Phe
230		235	240
Cys Ser Gly Ser	Cys Tyr Cys Pro Val	Arg Asn Gln Tyr Leu	Glu
245		250	255
Lys Glu Gln Arg	Arg Gln Tyr Leu Leu	Arg Leu Lys Asn Ser	Gln
260		265	270
Leu Glu Lys Thr	Tyr Gly Glu Met Ala	Lys Ile Val Asp Val	Pro
275		280	285
Thr Lys Gln Leu	Arg Ala Ala Asn Pro	Ile Asp Ser Met Leu	Cys
290		295	300
His Phe Cys His	Asn Val Ser Phe Pro	Cys Thr Arg Asn Gly	Cys
305		310	315
Val Asp Met Glu	His Phe Lys Val Ile	Lys Thr His Gln Ile	Glu
320		325	330
Asp Glu Arg Glu	Arg Arg Glu Lys Lys	Leu Tyr Phe Gly Tyr	Ser
335		340	345
Leu Leu Gly Ala	His Pro Ile Leu Asn	Gln Thr Ile Gly Arg	Met
350		355	360
Gln Arg Ala Thr	Glu Gly Arg Lys Glu	Glu Leu Phe Ala Leu	Tyr
365		370	375
Ser Ala His Asp	Val Thr Leu Ser Pro	Val Leu Ser Ala Leu	Gly
380		385	390
Leu Ser Glu Ala	Arg Phe Pro Arg Phe	Ala Ala Arg Leu Ile	Phe
395		400	405
Glu Leu Trp Gln	Asp Arg Glu Lys Pro	Ser Glu His Ser Val	Arg
410		415	420
Ile Leu Tyr Asn	Gly Val Asp Val Thr	Phe His Thr Ser Phe	Cys
425		430	435
Gln Asp His His	Lys Arg Ser Pro Lys	Pro Met Cys Pro Leu	Glu
440		445	450
Asn Leu Val Arg	Phe Val Lys Arg Asp	Met Phe Val Ala Leu	Gly
455		460	465
Gly Ser Gly Thr	Asn Tyr Tyr Asp Ala	Cys His Arg Glu Gly	Phe
470		475	480

<210> 386  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 386  
ccaagcagct tagagctcca gacc 24

<210> 387  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 387  
ttccctatgc tctgtattgg catgg 25

<210> 388  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 388  
gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389  
<211> 3313  
<212> DNA  
<213> Homo sapiens

<400> 389  
aaaaaagctc actaaagttt ctattagagc gaatacggta gatttccatc 50  
cccttttgaa gaacagtact gtggagctat ttaagagata aaaacgaaat 100  
atcctttctg ggagttcaag attgtgcagt aattgggttag gactctgagc 150  
gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200  
cacgcgcttg aagcacaaaag cagatagcta ggaatgaacc atccctggga 250  
gtatgtggaa acaacggagg agctctgact tccaactgt ccattctat 300  
gggcgaagga actgctcctg acttcagtgg ttaagggcag aattgaaaat 350  
aattctggag gaagataaga atgattcctg cgcgactgca ccgggactac 400  
aaagggcttg tcctgctggg aatcctcctg gggactctgt gggagaccgg 450  
atgcaccag atacgtatt cagttccgga agagctggag aaaggctcta 500  
gggtgggcga catctccagg gacctggggc tggagccccg ggagctcgcg 550  
gagcgcggag tccgcatcat cccagaggt aggacgcagc ttttcgcct 600







Met	Ile	Pro	Ala	Arg	Leu	His	Arg	Asp	Tyr	Lys	Gly	Leu	Val	Leu	1	5	10	15
Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln	20	25	30	
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu	110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	275	280	285	
Asp	Lys	Ala	Ala	Gln	Val	Phe	Lys	Leu	Asp	Cys	Asn	Ser	Gly	Thr				

TOP201-1302100

	290		295		300
Ile Ser Thr Ile	Gly Glu Leu Asp His	Glu Glu Ser Gly Phe Tyr			
	305	310			315
Gln Met Glu Val	Gln Ala Met Asp Asn	Ala Gly Tyr Ser Ala Arg			
	320	325			330
Ala Lys Val Leu	Ile Thr Val Leu Asp	Val Asn Asp Asn Ala Pro			
	335	340			345
Glu Val Val Leu	Thr Ser Leu Ala Ser	Ser Val Pro Glu Asn Ser			
	350	355			360
Pro Arg Gly Thr	Leu Ile Ala Leu Leu	Asn Val Asn Asp Gln Asp			
	365	370			375
Ser Glu Glu Asn	Gly Gln Val Ile Cys	Phe Ile Gln Gly Asn Leu			
	380	385			390
Pro Phe Lys Leu	Glu Lys Ser Tyr Gly	Asn Tyr Tyr Ser Leu Val			
	395	400			405
Thr Asp Ile Val	Leu Asp Arg Glu Gln	Val Pro Ser Tyr Asn Ile			
	410	415			420
Thr Val Thr Ala	Thr Asp Arg Gly Thr	Pro Pro Leu Ser Thr Glu			
	425	430			435
Thr His Ile Ser	Leu Asn Val Ala Asp	Thr Asn Asp Asn Pro Pro			
	440	445			450
Val Phe Pro Gln	Ala Ser Tyr Ser Ala	Tyr Ile Pro Glu Asn Asn			
	455	460			465
Pro Arg Gly Val	Ser Leu Val Ser Val	Thr Ala His Asp Pro Asp			
	470	475			480
Cys Glu Glu Asn	Ala Gln Ile Thr Tyr	Ser Leu Ala Glu Asn Thr			
	485	490			495
Ile Gln Gly Ala	Ser Leu Ser Ser Tyr	Val Ser Ile Asn Ser Asp			
	500	505			510
Thr Gly Val Leu	Tyr Ala Leu Ser Ser	Phe Asp Tyr Glu Gln Phe			
	515	520			525
Arg Asp Leu Gln	Val Lys Val Met Ala	Arg Asp Asn Gly His Pro			
	530	535			540
Pro Leu Ser Ser	Asn Val Ser Leu Ser	Leu Phe Val Leu Asp Gln			
	545	550			555
Asn Asp Asn Ala	Pro Glu Ile Leu Tyr	Pro Ala Leu Pro Thr Asp			
	560	565			570
Gly Ser Thr Gly	Val Glu Leu Ala Pro	Arg Ser Ala Glu Pro Gly			
	575	580			585



875

880

885

Ser Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp  
890 895 900

Glu Ala Glu Ala Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro  
905 910 915

Ala

&lt;210&gt; 391

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 391

tccgtctctg tgaaccgccc cac 23

&lt;210&gt; 392

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 392

ctcgggcgca ttgtcgttct ggtc 24

&lt;210&gt; 393

&lt;211&gt; 40

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 393

ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

&lt;210&gt; 394

&lt;211&gt; 999

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 394

cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50

cccagttaaa aggctccaga atcgtgtacc aggcagagaa ctgaagtact 100

ggggcctcct ccaactgggtc cgaatcagta ggtgaccccg cccttgatt 150

ctggaagacc tcaccatggg acgccccga cctcgtgcgg ccaagacgtg 200

gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250  
 aggaggacaa ggtgctgggg ggtcatgagt gccaacccca ttcgcagcct 300  
 tggcaggcgg ccttgttcca gggccagcaa ctactctgtg gcggtgtcct 350  
 tgtaggtggc aactgggtcc ttacagctgc ccactgtaaa aaaccgaaat 400  
 acacagtacg cctgggagac cacagcctac agaataaaga tggcccagag 450  
 caagaataac ctgtggttca gtccatccca caccctgct acaacagcag 500  
 cgatgtggag gaccacaacc atgatctgat gcttcttcaa ctgcgtgacc 550  
 aggcacocct ggggtccaaa gtgaagccca tcagcctggc agatcattgc 600  
 acccagcctg gccagaagtg caccgtctca ggctggggca ctgtcaccag 650  
 tccccgagag aattttcctg acactctcaa ctgtgcagaa gtaaaaatct 700  
 ttccccagaa gaagtgtgag gatgcttacc cggggcagat cacagatggc 750  
 atggtctgtg caggcagcag caaaggggct gacacgtgcc agggcgattc 800  
 tggaggcccc ctggtgtgtg atggtgcaact ccagggcata acatcctggg 850  
 gctcagaccc ctgtgggagg tccgacaaac ctggcgtcta taccaacata 900  
 tgccgctacc tggactggat caagaagatc ataggcagca agggctgatt 950  
 ctaggataag cactagatct cccttaataa actcacaact ctctggttc 999

<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Ala	Lys	Thr	Trp	Met	Phe	Leu
1				5					10					15
Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30
Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
			35						40					45
Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
			50						55					60
Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
			65						70					75
Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn
			80						85					90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro
			95						100					105

His Pro Cys Tyr Asn Ser Ser Asp Val Glu Asp His Asn His Asp  
 110 115 120  
 Leu Met Leu Leu Gln Leu Arg Asp Gln Ala Ser Leu Gly Ser Lys  
 125 130 135  
 Val Lys Pro Ile Ser Leu Ala Asp His Cys Thr Gln Pro Gly Gln  
 140 145 150  
 Lys Cys Thr Val Ser Gly Trp Gly Thr Val Thr Ser Pro Arg Glu  
 155 160 165  
 Asn Phe Pro Asp Thr Leu Asn Cys Ala Glu Val Lys Ile Phe Pro  
 170 175 180  
 Gln Lys Lys Cys Glu Asp Ala Tyr Pro Gly Gln Ile Thr Asp Gly  
 185 190 195  
 Met Val Cys Ala Gly Ser Ser Lys Gly Ala Asp Thr Cys Gln Gly  
 200 205 210  
 Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Ala Leu Gln Gly Ile  
 215 220 225  
 Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser Asp Lys Pro Gly  
 230 235 240  
 Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile Lys Lys Ile  
 245 250 255  
 Ile Gly Ser Lys Gly  
 260

<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gccc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccatcccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

ggcgccggtg caccgggcgg gctgagcgcc tcctgcggcc cggcctgcgc 50

gccccggccc gccgcgccgc ccacgcccc accccggccc gcgcccccta 100

gccccgccc gggcccgcgc ccgcgcccgc gccagggtga gcgctccgcc 150

cgccgcgagg ccccgccccg gcccgcccc gcccgcccc ggccggcggg 200

ggaaccgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250

tcatoctccc ggcgccccgc gctgcgagcg ccccgccagt ccgcgcgcgc 300

gccgccctcg cctgtgcgc cctgcgcgcc ctgcgcaccc gcggcccgag 350

cccagccaga gccgggcgga gcggagcgcg ccgagcctcg tcccgcggcc 400

gggcgggggc cgggccgtag cggcggcgcc tggatgcgga cccggccgcg 450

gggagacggg cggccgcccc gaaacgactt tcagtccccg acgcgccccg 500

cccaaccct acgatgaaga gggcgtccgc tggaggagc cggtgctgg 550

catgggtgct gtggctgcag gcctggcagg tggcagcccc atgccagggt 600

gcctgcgtat gctacaatga gcccaagggt acgacaagct gccccagca 650

gggcctgcag gctgtgcccg tgggcatccc tgctgccagc cagcgcatt 700

tcctgcacgg caaccgcatc tcgcatgtgc cagctgccag cttccgtgcc 750

tgccgcaacc tcaccatcct gtggctgcac tcgaatgtgc tggcccgaa 800

tgatgcggct gccttactg gcctggccct cctggagcag ctggacctca 850

gcgataatgc acagctccg tctgtggacc ctgccacatt ccacggcctg 900

ggcgcctac acacgtgca cctggaccgc tgcggcctgc aggagctggg 950

cccggggctg ttccgcggcc tggctgcct gcagtacct tacctgcagg 1000

acaacgcgt gcaggcactg cctgatgaca cttccgcga cctgggcaac 1050

ctcacacacc tcttctgca cggcaaccgc atctccagcg tgcccagcg 1100

ccggttcctg







320	325	330
Gly Leu Pro Lys Cys Cys Gln Pro Asp	Ala Ala Asp Lys Ala Ser	
335	340	345
Val Leu Glu Pro Gly Arg Pro Ala Ser	Ala Gly Asn Ala Leu Lys	
350	355	360
Gly Arg Val Pro Pro Gly Asp Ser Pro	Pro Gly Asn Gly Ser Gly	
365	370	375
Pro Arg His Ile Asn Asp Ser Pro Phe	Gly Thr Leu Pro Gly Ser	
380	385	390
Ala Glu Pro Pro Leu Thr Ala Val Arg	Pro Glu Gly Ser Glu Pro	
395	400	405
Pro Gly Phe Pro Thr Ser Gly Pro Arg	Arg Arg Pro Gly Cys Ser	
410	415	420
Arg Lys Asn Arg Thr Arg Ser His Cys	Arg Leu Gly Gln Ala Gly	
425	430	435
Ser Gly Gly Gly Gly Thr Gly Asp Ser	Glu Gly Ser Gly Ala Leu	
440	445	450
Pro Ser Leu Thr Cys Ser Leu Thr Pro	Leu Gly Leu Ala Leu Val	
455	460	465
Leu Trp Thr Val Leu Gly Pro Cys		
470		

<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggtgcacct gcagtacctc tacc 24

<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

ggaagtccac ggggagcttg gatgccaaag ggaggacggc tgggtcctct 50

ggagaggact actcactggc atatttctga ggtatctgta gaataaccac 100

agcctcagat actggggact ttacagtccc acagaaccgt cctcccagga 150

agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgaga 200

caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250

cgcgggcgga cctagaagct attctgtggt ggaggaaact gagggcagct 300

cctttgtcac caatttagca aaggacctgg gtctggagca gagggaattc 350

tccaggcggg gggttagggt tgtttcagga gggaacaaac tacatttgca 400

gctcaatcag gagaccgcgg atttgttgct aaatgagaaa ttggaccgtg 450

aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500

ctagagagtc ccttcgagtt ttttcaagct gagctgcaag taatagacat 550

aaacgaccac tctccagtat ttctggacaa acaaagtgtg gtgaaagtat 600

cagagagcag tcctcctggg actacgtttc ctctgaagaa tgccgaagac 650

ttagatgtag gccaaaacaa tattgagaac tatataatca gcccactc 700

ctattttcgg gtcctcacc gcaaacgcag tgatggcagg aaatacccag 750

agctggtgct ggacaaagcg ctggaccgag aggaagaagc tgagctcagg 800

ttaacactca cagcactgga tgggtggtct ccgccagat ctggcactgc 850

tcaggtctac atcgaagtcc tggatgtcaa cgataatgcc cctgaatttg 900

agcagccttt ctatagagtg cagatctctg aggacagtcc ggtaggcttc 950

ctggttggtga aggtctctgc cacggatgta gacacaggag tcaacggaga 1000

gatttcctat tcacttttcc aagcttcaga agagattggc aaaaccttta 1050

agatcaatcc cttgacagga gaaattgaac taaaaaaca actcgatttc 1100

gaaaaacttc agtcctatga agtcaatatt gaggcaagag atgctggaac 1150

sequence: 180CTDDE

cttttctgga aaatgcaccg ttctgattca agtgatagat gtgaacgacc 1200  
 atgccccaga agttaccatg tctgcattta ccagcccaat acctgagaac 1250  
 gcgcctgaaa ctgtggttgc acttttcagt gtttcagatc ttgattcagg 1300  
 agaaaatggg aaaattagtt gctccattca ggaggatcta cccttcctcc 1350  
 tgaaatccgc ggaaaacttt tacaccctac taacggagag accactagac 1400  
 agagaaagca gagcggaata caacatcact atcactgtca ctgacttggt 1450  
 gaccocctatg ctgataacac agctcaatat gaccgtgctg atcgccgatg 1500  
 tcaatgacaa cgctcccgcg ttcacccaaa cctcctacac cctgttcgtc 1550  
 gcgcgagaaca acagccccgc cctgcacatc cgcagcgtca gcgctacaga 1600  
 cagagactca ggcaccaacg cccaggtcac ctactcgtg ctgccgcccc 1650  
 aggacccgca cctgcccctc acatccctgg tctccatcaa cgcggacaac 1700  
 ggccacctgt tcgccctcag gtctctggac tacgaggccc tgcagggtt 1750  
 ccagttccgc gtgggcgctt cagaccacgg ctccccggcg ctgagcagcg 1800  
 aggcgctggt gcgcgtggtg gtgctggacg ccaacgacaa ctgcccttc 1850  
 gtgctgtacc cgctgcagaa cggctccgcg ccctgcaccg agctggtgcc 1900  
 ccgggcggcc gagccgggct acctggtgac caaggtggtg gcggtggacg 1950  
 gcgactcggg ccagaacgcc tggctgtcgt accagctgct caaggccacg 2000  
 gagctcggtc tgttcggcgt gtgggcgcac aatggcgagg tgcgcaccgc 2050  
 caggctgctg agcgagcgcg acgcggccaa gcacaggctg gtggtgctgg 2100  
 tcaaggacaa tggcgagcct ccgcgctcgg ccaccgccac gctgcacgtg 2150  
 ctctggtggt acggcttctc ccagccctac ctgcctctcc cggaggcggc 2200  
 cccgaccag gccagggccg acttgctcac cgtctacctg gtggtggcgt 2250  
 tggcctcggg gtcttcgctc ttctctttt cgggtgctct gttcgtggcg 2300  
 gtgcggctgt gtaggaggag cagggcggcc tcggtgggtc gctgcttgg 2350  
 gcccgagggc ccccttcag ggcattctgt ggacatgagc ggcaccagga 2400  
 ccctatccca gagctaccag tatgaggtgt gtctggcagg aggtcaggg 2450  
 accaatgagt tcaagttcct gaagccgatt atccccaact tccctcccca 2500  
 gtgccctggg aaagaaatac aaggaaattc taccttccc aataactttg 2550  
 ggttcaatat tcagtacca tagttgactt ttacattcca taggtatttt 2600

attttgtggc atttccatgc caatgtttat ttccccaat ttgtgtgtat 2650  
 gtaatatgt acggatttac tcttgatttt tctcatgttc tttctccctt 2700  
 tgttttaag tgaacattta cctttattcc tgggtctt 2738

<210> 405  
 <211> 798  
 <212> PRT  
 <213> Homo sapiens

<400> 405

Met Glu Ala Ser Gly Lys Leu Ile Cys Arg Gln Arg Gln Val Leu  
 1 5 10 15

Phe Ser Phe Leu Leu Leu Gly Leu Ser Leu Ala Gly Ala Ala Glu  
 20 25 30

Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe  
 35 40 45

Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe  
 50 55 60

Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His  
 65 70 75

Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Leu Asn Glu Lys  
 80 85 90

Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu  
 95 100 105

Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala  
 110 115 120

Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu  
 125 130 135

Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly  
 140 145 150

Thr Thr Phe Pro Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln  
 155 160 165

Asn Asn Ile Glu Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg  
 170 175 180

Val Leu Thr Arg Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu  
 185 190 195

Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg  
 200 205 210

Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly  
 215 220 225

Thr Ala Gln Val Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala

230	235	240
Pro Glu Phe Glu Gln Pro Phe Tyr Arg	Val Gln Ile Ser Glu Asp	
245	250	255
Ser Pro Val Gly Phe Leu Val Val Lys	Val Ser Ala Thr Asp Val	
260	265	270
Asp Thr Gly Val Asn Gly Glu Ile Ser	Tyr Ser Leu Phe Gln Ala	
275	280	285
Ser Glu Glu Ile Gly Lys Thr Phe Lys	Ile Asn Pro Leu Thr Gly	
290	295	300
Glu Ile Glu Leu Lys Lys Gln Leu Asp	Phe Glu Lys Leu Gln Ser	
305	310	315
Tyr Glu Val Asn Ile Glu Ala Arg Asp	Ala Gly Thr Phe Ser Gly	
320	325	330
Lys Cys Thr Val Leu Ile Gln Val Ile	Asp Val Asn Asp His Ala	
335	340	345
Pro Glu Val Thr Met Ser Ala Phe Thr	Ser Pro Ile Pro Glu Asn	
350	355	360
Ala Pro Glu Thr Val Val Ala Leu Phe	Ser Val Ser Asp Leu Asp	
365	370	375
Ser Gly Glu Asn Gly Lys Ile Ser Cys	Ser Ile Gln Glu Asp Leu	
380	385	390
Pro Phe Leu Leu Lys Ser Ala Glu Asn	Phe Tyr Thr Leu Leu Thr	
395	400	405
Glu Arg Pro Leu Asp Arg Glu Ser Arg	Ala Glu Tyr Asn Ile Thr	
410	415	420
Ile Thr Val Thr Asp Leu Gly Thr Pro	Met Leu Ile Thr Gln Leu	
425	430	435
Asn Met Thr Val Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro Ala	
440	445	450
Phe Thr Gln Thr Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn Ser	
455	460	465
Pro Ala Leu His Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp Ser	
470	475	480
Gly Thr Asn Ala Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln Asp	
485	490	495
Pro His Leu Pro Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp Asn	
500	505	510
Gly His Leu Phe Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu Gln	
515	520	525

Gly Phe Gln Phe Arg Val Gly Ala Ser	Asp His Gly Ser Pro Ala	530	535	540
Leu Ser Ser Glu Ala Leu Val Arg Val	Val Val Leu Asp Ala Asn	545	550	555
Asp Asn Ser Pro Phe Val Leu Tyr Pro	Leu Gln Asn Gly Ser Ala	560	565	570
Pro Cys Thr Glu Leu Val Pro Arg Ala	Ala Glu Pro Gly Tyr Leu	575	580	585
Val Thr Lys Val Val Ala Val Asp Gly	Asp Ser Gly Gln Asn Ala	590	595	600
Trp Leu Ser Tyr Gln Leu Leu Lys Ala	Thr Glu Leu Gly Leu Phe	605	610	615
Gly Val Trp Ala His Asn Gly Glu Val	Arg Thr Ala Arg Leu Leu	620	625	630
Ser Glu Arg Asp Ala Ala Lys His Arg	Leu Val Val Leu Val Lys	635	640	645
Asp Asn Gly Glu Pro Pro Arg Ser Ala	Thr Ala Thr Leu His Val	650	655	660
Leu Leu Val Asp Gly Phe Ser Gln Pro	Tyr Leu Pro Leu Pro Glu	665	670	675
Ala Ala Pro Thr Gln Ala Gln Ala Asp	Leu Leu Thr Val Tyr Leu	680	685	690
Val Val Ala Leu Ala Ser Val Ser Ser	Leu Phe Leu Phe Ser Val	695	700	705
Leu Leu Phe Val Ala Val Arg Leu Cys	Arg Arg Ser Arg Ala Ala	710	715	720
Ser Val Gly Arg Cys Leu Val Pro Glu	Gly Pro Leu Pro Gly His	725	730	735
Leu Val Asp Met Ser Gly Thr Arg Thr	Leu Ser Gln Ser Tyr Gln	740	745	750
Tyr Glu Val Cys Leu Ala Gly Gly Ser	Gly Thr Asn Glu Phe Lys	755	760	765
Phe Leu Lys Pro Ile Ile Pro Asn Phe	Pro Pro Gln Cys Pro Gly	770	775	780
Lys Glu Ile Gln Gly Asn Ser Thr Phe	Pro Asn Asn Phe Gly Phe	785	790	795

Asn Ile Gln

<210> 406

<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 406  
ctgagaacgc gcctgaaact gtg 23

<210> 407  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 407  
agcgttgtca ttgacatcgg cg 22

<210> 408  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 408  
ttagtgtgtc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409  
<211> 1379  
<212> DNA  
<213> Homo sapiens

<400> 409  
accacgcgt ccgcccacgc gtccgccac gcgtccgcc acgcgtccgc 50  
gcgtagccgt gcgccgattg cctctcggcc tgggcaatgg tcccggctgc 100  
cggtcgacga ccgccccgcg tcattcggct cctcggctgg tggcaagtat 150  
tgctgtgggt gctgggactt ccggtccgcg gcgtggaggt tgcagaggaa 200  
agtggtcgct tatggtcaga ggagcagcct gtcaccctc tccaggtggg 250  
ggctgtgtac ctgggtgagg aggagctcct gcatgaccg atgggccagg 300  
acagggcagc agaagaggcc aatgcggtgc tggggctgga cacccaaggc 350  
gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400  
gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450  
caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500



cacttccctg acagagaaga ggagtattac acagagccag aagtggcgga 550  
 atctgacgca gccccgacag aggactccaa taactactgaa agtctgaaat 600  
 ccccaaaggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650  
 actctgaaaa ttttaaatat gtcacaggac cttatggatt ttctgaaccc 700  
 aaacggtagt gactgtactc tagtcctggt ttacaccccg tgggtgccgct 750  
 tttctgccag tttggccct cactttaact ctctgccccg ggcatittcca 800  
 gctcttcact ttttggcact ggatgcatct cagcacagca gcctttctac 850  
 caggtttggc accgtagctg ttcctaatat tttattattt caaggagcta 900  
 aaccaatggc cagatttaac catacagatc gaacactgga aacactgaaa 950  
 atcttcattt ttaatcagac aggtatagaa gccagaaga atgtggtggt 1000  
 aactcaagcc gaccaaatac gccctcttcc cagcactttg ataaaaagt 1050  
 tggactggtt gcttgtattt tccttattct ttttaattag ttttattatg 1100  
 tatgctacca ttcgaactga gagtattcgg tggctaattc caggacaaga 1150  
 gcaggaacat gtggagtagt gatggtctga aagaagttgg aaagaggaac 1200  
 ttcaatcctt cgtttcagaa attagtgcga cagtttcata cattttctcc 1250  
 agtgacgtgt tgacttgaaa cttcaggcag attaaaagaa tcatttggtg 1300  
 aacaactgaa tgtataaaaa aattataaac tgggtgttta actagtattg 1350  
 caataagcaa atgcaaaaat attcaatag 1379

<210> 410  
 <211> 360  
 <212> PRT  
 <213> Homo sapiens

<400> 410  
 Met Val Pro Ala Ala Gly Arg Arg Pro Pro Arg Val Met Arg Leu  
 1 5 10 15  
 Leu Gly Trp Trp Gln Val Leu Leu Trp Val Leu Gly Leu Pro Val  
 20 25 30  
 Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser Glu  
 35 40 45  
 Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly  
 50 55 60  
 Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala  
 65 70 75  
 Glu Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His

TOH204-188C-1004

	80		85		90
Met Val Met Leu Ser Val Ile Pro Gly	95	Glu Ala Glu Asp Lys Val	100		105
Ser Ser Glu Pro Ser Gly Val Thr Cys	110	Gly Ala Gly Gly Ala Glu	115		120
Asp Ser Arg Cys Asn Val Arg Glu Ser	125	Leu Phe Ser Leu Asp Gly	130		135
Ala Gly Ala His Phe Pro Asp Arg Glu	140	Glu Glu Tyr Tyr Thr Glu	145		150
Pro Glu Val Ala Glu Ser Asp Ala Ala	155	Pro Thr Glu Asp Ser Asn	160		165
Asn Thr Glu Ser Leu Lys Ser Pro Lys	170	Val Asn Cys Glu Glu Arg	175		180
Asn Ile Thr Gly Leu Glu Asn Phe Thr	185	Leu Lys Ile Leu Asn Met	190		195
Ser Gln Asp Leu Met Asp Phe Leu Asn	200	Pro Asn Gly Ser Asp Cys	205		210
Thr Leu Val Leu Phe Tyr Thr Pro Trp	215	Cys Arg Phe Ser Ala Ser	220		225
Leu Ala Pro His Phe Asn Ser Leu Pro	230	Arg Ala Phe Pro Ala Leu	235		240
His Phe Leu Ala Leu Asp Ala Ser Gln	245	His Ser Ser Leu Ser Thr	250		255
Arg Phe Gly Thr Val Ala Val Pro Asn	260	Ile Leu Leu Phe Gln Gly	265		270
Ala Lys Pro Met Ala Arg Phe Asn His	275	Thr Asp Arg Thr Leu Glu	280		285
Thr Leu Lys Ile Phe Ile Phe Asn Gln	290	Thr Gly Ile Glu Ala Lys	295		300
Lys Asn Val Val Val Thr Gln Ala Asp	305	Gln Ile Gly Pro Leu Pro	310		315
Ser Thr Leu Ile Lys Ser Val Asp Trp	320	Leu Leu Val Phe Ser Leu	325		330
Phe Phe Leu Ile Ser Phe Ile Met Tyr	335	Ala Thr Ile Arg Thr Glu	340		345
Ser Ile Arg Trp Leu Ile Pro Gly Gln	350	Glu Gln Glu His Val Glu	355		360

<210> 411  
 <211> 24

<212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic oligonucleotide probe

<400> 411  
 cacagagcca gaagtggcgg aatc 24

<210> 412  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 412  
 ccacatgttc ctgctcttgt cctgg 25

<210> 413  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 413  
 cggtagtgac tgtactctag tcctgtttta caccocgtgg tgccg 45

<210> 414  
 <211> 1196  
 <212> DNA  
 <213> Homo sapiens

<400> 414  
 cccggctccg ctccctctgc cccctcgggg tcgcgcgcc acgatgctgc 50  
 agggccctgg ctgcgtgctg ctgctcttcc tcgcctcgca ctgctgcctg 100  
 ggctcggcgc gcggtctctt cctctttggc cagcccgact tctcctacaa 150  
 gcgcagcaat tgcaagcca tcccggtaaa cctgcagctg tgccacggca 200  
 tcgaatacca gaacatgcgg ctgccaacc tgctgggcca cgagaccatg 250  
 aaggaggtgc tggagcaggc cggcgtttgg atcccgtgg tcatgaagca 300  
 gtgccaccgc gacaccaaga agttcctgtg ctgcctcttc gccccgtct 350  
 gcctcgatga cctagacgag accatccagc catgccactc gctctgcgtg 400  
 caggtgaagg accgctgcgc cccggtcatg tccgccttcg gttcccttg 450  
 gcccgacatg cttgagtgcg accgtttccc ccaggacaac gacctttgca 500  
 tccccctcgc tagcagcgac cacctcctgc cagccaccga ggaagctcca 550

aaggatgtg aagcctgcaa aaataaaaat gatgatgaca acgacataat 600  
ggaaacgctt tgtaaaaatg attttgact gaaaataaaa gtgaaggaga 650  
taacctacat caaccgagat accaaaatca tcctggagac caagagcaag 700  
accatttaca agctgaacgg tgtgtccgaa agggacctga agaaatcgg 750  
gctgtggctc aaagacagct tgcagtgcac ctgtgaggag atgaacgaca 800  
tcaacgcgcc ctatctggtc atgggacaga aacaggggtg ggagctggtg 850  
atcacctcgg tgaagcgggtg gcagaagggg cagagagagt tcaagcgc 900  
ctcccgagc atccgcaagc tgcagtgcta gtcccgcat cctgatggct 950  
ccgacaggcc tgctccagag cacggctgac catttctgct ccgggatctc 1000  
agctcccgtt cccaagcac actcctagct gctccagtct cagcctgggc 1050  
agcttcccc tgccttttgc acgtttgcat cccagcatt tcctgagtta 1100  
taaggccaca ggagtggata gctgttttca cctaaaggaa aagcccaccc 1150  
gaatcttgta gaaatattca aactaataaa atcatgaata ttttaa 1196

<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

Met	Leu	Gln	Gly	Pro	Gly	Ser	Leu	Leu	Leu	Leu	Phe	Leu	Ala	Ser	1	5	10	15
His	Cys	Cys	Leu	Gly	Ser	Ala	Arg	Gly	Leu	Phe	Leu	Phe	Gly	Gln	20	25	30	
Pro	Asp	Phe	Ser	Tyr	Lys	Arg	Ser	Asn	Cys	Lys	Pro	Ile	Pro	Val	35	40	45	
Asn	Leu	Gln	Leu	Cys	His	Gly	Ile	Glu	Tyr	Gln	Asn	Met	Arg	Leu	50	55	60	
Pro	Asn	Leu	Leu	Gly	His	Glu	Thr	Met	Lys	Glu	Val	Leu	Glu	Gln	65	70	75	
Ala	Gly	Ala	Trp	Ile	Pro	Leu	Val	Met	Lys	Gln	Cys	His	Pro	Asp	80	85	90	
Thr	Lys	Lys	Phe	Leu	Cys	Ser	Leu	Phe	Ala	Pro	Val	Cys	Leu	Asp	95	100	105	
Asp	Leu	Asp	Glu	Thr	Ile	Gln	Pro	Cys	His	Ser	Leu	Cys	Val	Gln	110	115	120	
Val	Lys	Asp	Arg	Cys	Ala	Pro	Val	Met	Ser	Ala	Phe	Gly	Phe	Pro	125	130	135	



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

ctcttcctct ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419

<211> 1830

<212> DNA

<213> Homo sapiens

<400> 419

gtggaggccg ccgacgatgg cggggccgac ggaggccgag acgggggttg 50

ccgagccccg ggcctgtgc gcgcagcggg gccaccgcac ctacgcgcgc 100

cgctgggtgt tctgtctgc gatcagcctg ctcaactgct ccaacgccac 150

gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200

tcctgtocat ggagcagatc aactggctgt cactggtcta cctcgtggta 250

tccaccccat ttggcgtggc ggccatctgg atcctggact ccgtcgggct 300

ccgtgcggcg accatcctgg gtgcgtggct gaactttgcc gggagtgtgc 350

tacgcatggt gccctgcatg gttgttggga cccaaaaccc atttgccttc 400

ctcatgggtg gccagagcct ctgtgccctt gccagagcc tggatcatctt 450

ctctccagcc aagctggctg ccttgtggtt cccagagcac cagcagacca 500

cggccaacat gctcgccacc atgtcgaacc ctctgggcgt ccttgtggcc 550

aatgtgctgt cccctgtgct ggtcaagaag ggtgaggaca ttccgttaat 600

gctcgtgtgc tataccatcc ctgctggcgt cgtctgcctg ctgtccacca 650

tctgcctgtg ggagagtgtg cccccaccc cgccctctgc cggggctgcc 700

agctccacct cagagaagtt cctggatggg ctcaagctgc agtcatgtg 750

gaacaaggcc tatgtcatcc tggctgtgtg cttgggggga atgatcgga 800

tctctgccag cttctcagcc ctctggagc agatcctctg tgcaagcggc 850

cactccagtg ggttttcgg cctctgtggc gctctcttca tcacgtttgg 900

gatcctgggg gcactggctc tcggccccta tgtggaccgg accaagcact 950

tcactgaggc caccaagatt ggcctgtgcc tgttctctct ggccctgcgtg 1000

ccctttgcc tggtgtccca gctgcaggga cagacccttg ccctggctgc 1050

cacctgctcg ctgctcgggc tgtttggtt ctcggtgggc ccctggcca 1100

the "foot"

tggagttggc ggtcgagtgt tccttccccg tgggggaggg ggctgccaca 1150  
 ggcatgatct ttgtgctggg gcaggccgag ggaataactca tcatgctggc 1200  
 aatgacggca ctgactgtgc gacgctcgga gccgtccttg tccacctgcc 1250  
 agcaggggga ggatccactt gactggacag tgtctctgct gctgatggcc 1300  
 ggctgtgca ccttcttcag ctgcatcctg gcggtcttct tccacacccc 1350  
 ataccggcgc ctgcaggccg agtctgggga gccccctcc acccgtaacg 1400  
 ccgtgggagg cgagactca gggccgggtg tggaccgagg gggagcagga 1450  
 agggctgggg tcttggggcc cagcacggcg actccggagt gcacggcgag 1500  
 gggggcctcg ctagaggacc ccagagggcc cgggagcccc caccagcct 1550  
 gccaccgagc gactccccgt gcgcaaggcc cagcagccac cgacgcgcc 1600  
 tcccgccccg gcagactcgc aggcagggtc caagcgtcca ggtttattga 1650  
 cccggctggg tctcactcct ccttctcctc cccgtgggtg atcacgtagc 1700  
 tgagcgctt gtagtcagg ttgcccgcca catcgatgga ggcgaactgg 1750  
 aacatctggt ccacctgcgg gcggggcgga aagggtcct tgcgggctcc 1800  
 gggagcgaat tacaagcgcg cacctgaaaa 1830

<210> 420

<211> 560

<212> PRT

<213> Homo sapiens

<400> 420

Met Ala Gly Pro Thr Glu Ala Glu Thr Gly Leu Ala Glu Pro Arg  
1 5 10 15

Ala Leu Cys Ala Gln Arg Gly His Arg Thr Tyr Ala Arg Arg Trp  
20 25 30

Val Phe Leu Leu Ala Ile Ser Leu Leu Asn Cys Ser Asn Ala Thr  
35 40 45

Leu Trp Leu Ser Phe Ala Pro Val Ala Asp Val Ile Ala Glu Asp  
50 55 60

Leu Val Leu Ser Met Glu Gln Ile Asn Trp Leu Ser Leu Val Tyr  
65 70 75

Leu Val Val Ser Thr Pro Phe Gly Val Ala Ala Ile Trp Ile Leu  
80 85 90

Asp Ser Val Gly Leu Arg Ala Ala Thr Ile Leu Gly Ala Trp Leu  
95 100 105

Asn Phe Ala Gly Ser Val Leu Arg Met Val Pro Cys Met Val Val





Pro Ser Leu Ser Thr Cys Gln Gln Gly Glu Asp Pro Leu Asp Trp  
410 415 420

Thr Val Ser Leu Leu Leu Met Ala Gly Leu Cys Thr Phe Phe Ser  
425 430 435

Cys Ile Leu Ala Val Phe Phe His Thr Pro Tyr Arg Arg Leu Gln  
440 445 450

Ala Glu Ser Gly Glu Pro Pro Ser Thr Arg Asn Ala Val Gly Gly  
455 460 465

Ala Asp Ser Gly Pro Gly Val Asp Arg Gly Gly Ala Gly Arg Ala  
470 475 480

Gly Val Leu Gly Pro Ser Thr Ala Thr Pro Glu Cys Thr Ala Arg  
485 490 495

Gly Ala Ser Leu Glu Asp Pro Arg Gly Pro Gly Ser Pro His Pro  
500 505 510

Ala Cys His Arg Ala Thr Pro Arg Ala Gln Gly Pro Ala Ala Thr  
515 520 525

Asp Ala Pro Ser Arg Pro Gly Arg Leu Ala Gly Arg Val Gln Ala  
530 535 540

Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser  
545 550 555

Pro Trp Val Ile Thr  
560

<210> 421  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 421  
agcttctcag ccctcctgga gcag 24

<210> 422  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 422  
cggttcaata aacctggacg cttgg 25

<210> 423  
<211> 43  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 423

tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

gtccacatc ctgctcaact gggtcaggtc cctcttagac cagctcttgt 50  
ccatcatttg ctgaagtgga ccaactagtt cccagtagg gggctctccc 100  
tggcaattct tgatcggcgt ttggacatct cagatcgctt ccaatgaaga 150  
tggccttgcc ttggggctct gcttgtttca taatcatcta actatgggac 200  
aagggttgct cggcagctct gggggaagga gcacggggct gatcaagcca 250  
tccaggaaac actggaggac ttgtccagcc ttgaaagaac tctagtgggt 300  
tctgaatcta gccacttgg cggtaaagcat gatgcaactt ctgcaacttc 350  
tgctggggct tttggggcca ggtggctact tatttctttt aggggattgt 400  
caggaggtga ccactctcac ggtgaaatac caagtgtcag aggaagtgcc 450  
atctggtaca gtgatcggga agctgtccca ggaactgggc cgggaggaga 500  
ggcggaggca agctggggcc gccttcagg tgttgacgct gcctcaggcg 550  
ctccccattc aggtggactc tgaggaaggc ttgctcagca caggcaggcg 600  
gctggatcga gagcagctgt gccgacagt ggatccctgc ctggtttcct 650  
ttgatgtgct tgccacaggg gatttggtc tgatccatgt ggagatccaa 700  
gtgctggaca tcaatgacca ccagccacgg tttcccaaag gcgagcagga 750  
gctggaaatc tctgagagcg cctctctgcg aaccgggatc cccctggaca 800  
gagctcttga ccagacaca ggccctaaca ccctgcacac ctacactctg 850  
tctcccagtg agcactttgc cttggatgtc attgtgggcc ctgatgagac 900  
caaacatgca gaactcatag tggatgaagga gctggacagg gaaatccatt 950  
cattttttga tctggtgtta actgcctatg acaatgggaa ccccccaag 1000  
tcaggtaacca gcttgggtcaa ggtcaacgtc ttggactcca atgacaatag 1050  
ccctgcgttt gctgagagtt cactggcact ggaaatccaa gaagatgctg 1100

cacctggtac gtttctcata aaactgaccg ccacagaccc tgaccaaggc 1150  
 cccaatgggg aggtggagtt cttcctcagt aagcacatgc ctccagaggt 1200  
 gctggacacc ttcagtattg atgccaagac aggccaggtc attctgcgtc 1250  
 gacctctaga ctatgaaaag aaccctgcct acgaggtgga tgttcaggca 1300  
 agggacctgg gtccaatcc tatcccagcc cattgcaaag ttctcatcaa 1350  
 ggttctggat gtcaatgaca acatcccaag catccacgtc acatgggcct 1400  
 cccagccatc actggtgtca gaagctcttc ccaaggacag ttttattgct 1450  
 cttgtcatgg cagatgactt ggattcagga cacaatggtt tggtcactg 1500  
 ctggctgagc caagagctgg gccacttcag gctgaaaaga actaatggca 1550  
 acacatacat gttgctaacc aatgccacac tggacagaga gcagtggccc 1600  
 aaatataccc tcactctggt agcccaagac caaggactcc agcccttacc 1650  
 agccaagaaa cagctcagca ttcagatcag tgacatcaac gacaatgcac 1700  
 ctgtgtttga gaaaagcagg tatgaagtct ccacgcggga aaacaactta 1750  
 cctctcttc acctcattac catcaaggct catgatgcag acttgggcat 1800  
 taatggaaaa gtctcatacc gcatccagga ctcccagtt gctcacttag 1850  
 tagctattga ctccaacaca ggagaggtca ctgctcagag gtcactgaac 1900  
 tatgaagaga tggccggtt tgagttccag gtgatcgcag aggacagcgg 1950  
 gcaacccatg cttgcatcca gtgtctctgt gtgggtcagc ctcttggtg 2000  
 ccaatgataa tgccccagag gtgggtccagc ctgtgctcag cgatggaaaa 2050  
 gccagcctct cgtgtctgtt gaatgcctcc acaggccacc tgcgtgtgcc 2100  
 catcgagact cccaatggct tgggcccagc gggcactgac acacctccac 2150  
 tggccactca cagctcccgg ccattccttt tgacaacat tgtggcaaga 2200  
 gatgcagact cgggggcaaa tggagagccc ctctacagca tccgcaatgg 2250  
 aatgaagcc cacctcttca tcctcaacco tcatacggg cagctgttcg 2300  
 tcaatgtcac caatgccagc agcctcattg ggagtgagt ggagctggag 2350  
 atagtagtag aggaccaggg aagccccccc ttacagaccc gagccctgtt 2400  
 gagggcatg tttgtcacca gtgtggacca cctgagggac tcagcccga 2450  
 agcctggggc cttgagcatg tcgatgctga cggatgatct cctggctgta 2500  
 ctgttgggca tcttcgggtt gatcctggct ttgttcatgt ccactgtccg 2550

gacagaaaag aaggacaaca gggcctacaa ctgtcgggag gccgagtcca 2600  
cctaccgcca gcagcccaag aggccccaga aacacattca gaaggcagac 2650  
atccacctcg tgctgtgct caggggtcag gcaggtgagc cttgtgaagt 2700  
cgggcagtcc cacaagatg tggacaagga ggcgatgatg gaagcaggct 2750  
gggacccctg cctgcaggcc cccttccacc tcaccccgac cctgtacagg 2800  
acgctgcgta atcaaggcaa ccaggagca ccggcggaga gccgagaggt 2850  
gctgcaagac acggtcaacc tccttttcaa ccatcccagg cagaggaatg 2900  
cctcccgga gaacctgaac cttcccgagc ccagcctgc cacaggccag 2950  
ccacgttcca ggcctctgaa ggttgaggc agccccacag ggaggctggc 3000  
tggaagaccag ggcagtgagg aagccccaca gaggccacca gcctcctctg 3050  
caaccctgag acggcagcga catctcaatg gcaaagtgtc ccctgagaaa 3100  
gaatcagggc ccgctcagat cctgcggagc ctggccggc tgtctgtggc 3150  
tgccctcgcc gagcgaacc ccgtggagga gctcactgtg gattctctc 3200  
ctgttcagca aatctccag ctgctgtcct tgctgcatca gggccaattc 3250  
cagcccaaac caaaccaccg aggaaataag tacttgcca agccaggagg 3300  
cagcaggagt gcaatcccag acacagatgg cccaagtga agggctggag 3350  
gccagacaga ccagaaacag gaggaaggcc ctttgatcc tgaagaggac 3400  
ctctctgtga agcaactgct agaagaagag ctgtcaagtc tgctggaccc 3450  
cagcacaggt ctggccctgg accggctgag cgccctgac ccggcctgga 3500  
tggcgagact ctctttgccc ctcaccacca actaccgtga caatgtgatc 3550  
tccccggatg ctgcagccac ggaggagccg aggaccttc agacgttcgg 3600  
caaggcagag gcaccagagc tgagcccaac aggcacgagg ctggccagca 3650  
cctttgtctc ggagatgagc tcaactgctg agatgctgct ggaacagcgc 3700  
tccagcatgc ccgtggaggc cgcctccgag gcgctgcggc ggctctcgg 3750  
ctgcgggagg accctcagtt tagacttggc caccagtga gcctcaggca 3800  
tgaaagtga aggggaccca ggtggaaaga cggggactga gggcaagagc 3850  
agaggcagca gcagcagcag caggtgcctg tgaacatacc tcagacgcct 3900  
ctggatccaa gaaccagggg cctgaggatc tgtggacaag agctggtttc 3950  
taaaatcttg taactcacta gctagcggcg gcctgagaac tttagggtga 4000

ctgatgctac cccacagag gaggcaagag cccaggact aacagctgac 4050  
 tgaccaaagc agccccttgt aagcagctct gagtcttttg gaggacaggg 4100  
 acggtttgtg gctgagataa gtgtttcctg gcaaacata tgtggagcac 4150  
 aaagggtcag tcctctggca gaacagatgc cacggagtat cacaggcagg 4200  
 aaagggtggc cttcttgggt agcaggagtc agggggctgt accctggggg 4250  
 tgccaggaaa tgctctctga cctatcaata aaggaaaagc agtaaaaaaa 4300  
 aaaaaaaaaaaa aaa 4313

<210> 425

<211> 1184

<212> PRT

<213> Homo sapiens

<400> 425

Met	Met	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Gly	Leu	Leu	Gly	Pro	Gly	
1				5					10					15	
Gly	Tyr	Leu	Phe	Leu	Leu	Gly	Asp	Cys	Gln	Glu	Val	Thr	Thr	Leu	
				20					25					30	
Thr	Val	Lys	Tyr	Gln	Val	Ser	Glu	Glu	Val	Pro	Ser	Gly	Thr	Val	
				35					40					45	
Ile	Gly	Lys	Leu	Ser	Gln	Glu	Leu	Gly	Arg	Glu	Glu	Arg	Arg	Arg	
				50					55					60	
Gln	Ala	Gly	Ala	Ala	Phe	Gln	Val	Leu	Gln	Leu	Pro	Gln	Ala	Leu	
				65					70					75	
Pro	Ile	Gln	Val	Asp	Ser	Glu	Glu	Gly	Leu	Leu	Ser	Thr	Gly	Arg	
				80					85					90	
Arg	Leu	Asp	Arg	Glu	Gln	Leu	Cys	Arg	Gln	Trp	Asp	Pro	Cys	Leu	
				95					100					105	
Val	Ser	Phe	Asp	Val	Leu	Ala	Thr	Gly	Asp	Leu	Ala	Leu	Ile	His	
				110					115					120	
Val	Glu	Ile	Gln	Val	Leu	Asp	Ile	Asn	Asp	His	Gln	Pro	Arg	Phe	
				125					130					135	
Pro	Lys	Gly	Glu	Gln	Glu	Leu	Glu	Ile	Ser	Glu	Ser	Ala	Ser	Leu	
				140					145					150	
Arg	Thr	Arg	Ile	Pro	Leu	Asp	Arg	Ala	Leu	Asp	Pro	Asp	Thr	Gly	
				155					160					165	
Pro	Asn	Thr	Leu	His	Thr	Tyr	Thr	Leu	Ser	Pro	Ser	Glu	His	Phe	
				170					175					180	
Ala	Leu	Asp	Val	Ile	Val	Gly	Pro	Asp	Glu	Thr	Lys	His	Ala	Glu	
				185					190					195	

101201-1001

Leu Ile Val Val Lys Glu Leu Asp Arg Glu Ile His Ser Phe Phe  
200 205 210

Asp Leu Val Leu Thr Ala Tyr Asp Asn Gly Asn Pro Pro Lys Ser  
215 220 225

Gly Thr Ser Leu Val Lys Val Asn Val Leu Asp Ser Asn Asp Asn  
230 235 240

Ser Pro Ala Phe Ala Glu Ser Ser Leu Ala Leu Glu Ile Gln Glu  
245 250 255

Asp Ala Ala Pro Gly Thr Leu Leu Ile Lys Leu Thr Ala Thr Asp  
260 265 270

Pro Asp Gln Gly Pro Asn Gly Glu Val Glu Phe Phe Leu Ser Lys  
275 280 285

His Met Pro Pro Glu Val Leu Asp Thr Phe Ser Ile Asp Ala Lys  
290 295 300

Thr Gly Gln Val Ile Leu Arg Arg Pro Leu Asp Tyr Glu Lys Asn  
305 310 315

Pro Ala Tyr Glu Val Asp Val Gln Ala Arg Asp Leu Gly Pro Asn  
320 325 330

Pro Ile Pro Ala His Cys Lys Val Leu Ile Lys Val Leu Asp Val  
335 340 345

Asn Asp Asn Ile Pro Ser Ile His Val Thr Trp Ala Ser Gln Pro  
350 355 360

Ser Leu Val Ser Glu Ala Leu Pro Lys Asp Ser Phe Ile Ala Leu  
365 370 375

Val Met Ala Asp Asp Leu Asp Ser Gly His Asn Gly Leu Val His  
380 385 390

Cys Trp Leu Ser Gln Glu Leu Gly His Phe Arg Leu Lys Arg Thr  
395 400 405

Asn Gly Asn Thr Tyr Met Leu Leu Thr Asn Ala Thr Leu Asp Arg  
410 415 420

Glu Gln Trp Pro Lys Tyr Thr Leu Thr Leu Leu Ala Gln Asp Gln  
425 430 435

Gly Leu Gln Pro Leu Ser Ala Lys Lys Gln Leu Ser Ile Gln Ile  
440 445 450

Ser Asp Ile Asn Asp Asn Ala Pro Val Phe Glu Lys Ser Arg Tyr  
455 460 465

Glu Val Ser Thr Arg Glu Asn Asn Leu Pro Ser Leu His Leu Ile  
470 475 480

Thr Ile Lys Ala His Asp Ala Asp Leu Gly Ile Asn Gly Lys Val

	485	490	495
Ser Tyr Arg Ile	Gln Asp Ser Pro Val	Ala His Leu Val Ala	Ile
	500	505	510
Asp Ser Asn Thr	Gly Glu Val Thr Ala	Gln Arg Ser Leu Asn	Tyr
	515	520	525
Glu Glu Met Ala	Gly Phe Glu Phe Gln	Val Ile Ala Glu Asp	Ser
	530	535	540
Gly Gln Pro Met	Leu Ala Ser Ser Val	Ser Val Trp Val Ser	Leu
	545	550	555
Leu Asp Ala Asn	Asp Asn Ala Pro Glu	Val Val Gln Pro Val	Leu
	560	565	570
Ser Asp Gly Lys	Ala Ser Leu Ser Val	Leu Val Asn Ala Ser	Thr
	575	580	585
Gly His Leu Leu	Val Pro Ile Glu Thr	Pro Asn Gly Leu Gly	Pro
	590	595	600
Ala Gly Thr Asp	Thr Pro Pro Leu Ala	Thr His Ser Ser Arg	Pro
	605	610	615
Phe Leu Leu Thr	Thr Ile Val Ala Arg	Asp Ala Asp Ser Gly	Ala
	620	625	630
Asn Gly Glu Pro	Leu Tyr Ser Ile Arg	Asn Gly Asn Glu Ala	His
	635	640	645
Leu Phe Ile Leu	Asn Pro His Thr Gly	Gln Leu Phe Val Asn	Val
	650	655	660
Thr Asn Ala Ser	Ser Leu Ile Gly Ser	Glu Trp Glu Leu Glu	Ile
	665	670	675
Val Val Glu Asp	Gln Gly Ser Pro Pro	Leu Gln Thr Arg Ala	Leu
	680	685	690
Leu Arg Val Met	Phe Val Thr Ser Val	Asp His Leu Arg Asp	Ser
	695	700	705
Ala Arg Lys Pro	Gly Ala Leu Ser Met	Ser Met Leu Thr Val	Ile
	710	715	720
Cys Leu Ala Val	Leu Leu Gly Ile Phe	Gly Leu Ile Leu Ala	Leu
	725	730	735
Phe Met Ser Ile	Cys Arg Thr Glu Lys	Lys Asp Asn Arg Ala	Tyr
	740	745	750
Asn Cys Arg Glu	Ala Glu Ser Thr Tyr	Arg Gln Gln Pro Lys	Arg
	755	760	765
Pro Gln Lys His	Ile Gln Lys Ala Asp	Ile His Leu Val Pro	Val
	770	775	780

Leu Arg Gly Gln Ala Gly Glu Pro Cys Glu Val Gly Gln Ser His  
 785 790 795  
 Lys Asp Val Asp Lys Glu Ala Met Met Glu Ala Gly Trp Asp Pro  
 800 805 810  
 Cys Leu Gln Ala Pro Phe His Leu Thr Pro Thr Leu Tyr Arg Thr  
 815 820 825  
 Leu Arg Asn Gln Gly Asn Gln Gly Ala Pro Ala Glu Ser Arg Glu  
 830 835 840  
 Val Leu Gln Asp Thr Val Asn Leu Leu Phe Asn His Pro Arg Gln  
 845 850 855  
 Arg Asn Ala Ser Arg Glu Asn Leu Asn Leu Pro Glu Pro Gln Pro  
 860 865 870  
 Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser  
 875 880 885  
 Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro  
 890 895 900  
 Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His  
 905 910 915  
 Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln  
 920 925 930  
 Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu  
 935 940 945  
 Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln  
 950 955 960  
 Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln  
 965 970 975  
 Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly  
 980 985 990  
 Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg  
 995 1000 1005  
 Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp  
 1010 1015 1020  
 Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu  
 1025 1030 1035  
 Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu  
 1040 1045 1050  
 Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu  
 1055 1060 1065  
 Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala



1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala		
1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val		
1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser		
1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser		
1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala		
1145	1150	1155
Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr		
1160	1165	1170
Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Ser Arg Cys Leu		
1175	1180	

1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125 1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180

```

<210> 426
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 426
gtaagcacat gcctccagag gtgc 24

<210> 427
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 427
gtgacgtgga tgcttgggat gttg 24

<210> 428
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 428
tggacacctt cagtattgat gccaaagacag gccaggtcat tctgcgtcga 50

<210> 429
<211> 2037

```

<213> Homo sapiens

cggaacgcgtg	ggcggacgcg	tgggggagag	ccgcagtcgcc	ggctgcagca	50
cctgggagaa	ggcagaccgt	gtgagggggc	ctgtggcccc	agcgtgctgt	100
ggcctcgggg	agtgggaagt	ggaggcagga	gccttcctta	cacttcgcca	150
tgagtttcct	catcgactcc	agcatcatga	ttacctccca	gatactatgt	200
tttggatttg	ggtggctttt	cttcatgcgc	caattgttta	aagactatga	250
gatacgtcag	tatgttgtag	aggtgatctt	ctccgtgacg	tttgcatttt	300
cttgcaccat	gtttgagctc	atcatctttg	aaatcttagg	agtattgaat	350
agcagctccc	gttattttca	ctggaaaatg	aacctgtgtg	taattctgct	400
gatcctgggt	ttcatgggtg	ctttttacat	tggctatttt	attgtgagca	450
atatccgact	actgcataaa	caacgactgc	ttttttctg	tctcttatgg	500
ctgaccttta	tgtattttct	ctggaaaacta	ggagatccct	ttcccattct	550
cagcccaaaa	catgggatct	tatccataga	acagctcatc	agccggggtg	600
gtgtgattgg	agtgactctc	atggctcttc	tttctggatt	tgggtgctgc	650
aactgcccat	acacttacat	gtcttacttc	ctcaggaatg	tgactgacac	700
ggatattcta	gccctggaac	ggcgactgct	gcaaaccatg	gatatgatca	750
taagcaaaaa	gaaaaggatg	gcaatggcac	ggagaacaat	gttccagaag	800
ggggaagtgc	ataacaaacc	atcaggtttc	tggggaatga	taaaaagtgt	850
taccacttca	gcatcaggaa	gtgaaaatct	tactcttatt	caacaggaag	900
tggatgcttt	ggaagaatta	agcaggcagc	tttttctgga	aacagctgat	950
ctatatgcta	ccaaggagag	aatagaatac	tccaaaacct	tcaaggggaa	1000
atattttaat	tttcttggtt	actttttctc	tatttactgt	gtttggaaaa	1050
ttttcatggc	taccatcaat	attgtttttg	atcgagtgtg	gaaaacggat	1100
cctgtcacia	gaggcattga	gatcactgtg	aattatctgg	gaatccaatt	1150
tgatgtgaag	ttttgggtcc	aacacatttc	cttcattctt	gttggaaata	1200
tcacgtcac	atccatcaga	ggattgctga	tcactcttac	caagttcttt	1250
tatgccatct	ctagcagtaa	gtcctccaat	gtcattgtcc	tgctatttag	1300
acagataatg	ggcatgtact	ttgtctcctc	tgtgctgctg	atccgaatga	1350

gtatgccttt agaataccgc accataatca ctgaagtcct tggagaactg 1400  
 cagttcaact tctatcacgc ttggtttgat gtgatcttcc tggtcagcgc 1450  
 tctctctagc atactcttcc tctatttggc tcacaaacag gcaccagaga 1500  
 agcaaatggc accttgaact taagcctact acagactgtt agaggccagt 1550  
 ggtttcaaaa tttagatata agagggggga aaaatggaac cagggcctga 1600  
 cattttataa acaaacaaaa tgctatggta gcatttttca cttcatagc 1650  
 atactccttc cccgtcaggt gatactatga ccatgagtag catcagccag 1700  
 aacatgagag ggagaactaa ctcaagacaa tactcagcag agagcatccc 1750  
 gtgtggatat gaggctggtg tagaggcgga gaggagccaa gaaactaaag 1800  
 gtgaaaaata cactggaact ctggggcaag acatgtctat ggtagctgag 1850  
 ccaaacacgt aggatttccg ttttaagggt cacatggaaa aggttatagc 1900  
 tttgccttga gattgactca ttaaaatcag agactgtaac aaaaaaaaaa 1950  
 aaaaaaaaaa agggcgccgc cgactctaga gtcgacctgc agaagcttgg 2000  
 ccgccatggc ccaacttggt tattgcagct tataatg 2037

<210> 430

<211> 455

<212> PRT

<213> Homo sapiens

<400> 430

Met Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile  
 1 5 10 15

Leu Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe  
 20 25 30

Lys Asp Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser  
 35 40 45

Val Thr Phe Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe  
 50 55 60

Glu Ile Leu Gly Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp  
 65 70 75

Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val  
 80 85 90

Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu  
 95 100 105

His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe  
 110 115 120

Met Tyr Phe Phe Trp Lys Leu Gly Asp Pro Phe Pro Ile Leu Ser  
125 130 135

Pro Lys His Gly Ile Leu Ser Ile Glu Gln Leu Ile Ser Arg Val  
140 145 150

Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu Ser Gly Phe Gly  
155 160 165

Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe Leu Arg Asn  
170 175 180

Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu Leu Gln  
185 190 195

Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met Ala  
200 205 210

Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser  
215 220 225

Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly  
230 235 240

Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu  
245 250 255

Glu Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala  
260 265 270

Thr Lys Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr  
275 280 285

Phe Asn Phe Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys  
290 295 300

Ile Phe Met Ala Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys  
305 310 315

Thr Asp Pro Val Thr Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu  
320 325 330

Gly Ile Gln Phe Asp Val Lys Phe Trp Ser Gln His Ile Ser Phe  
335 340 345

Ile Leu Val Gly Ile Ile Ile Val Thr Ser Ile Arg Gly Leu Leu  
350 355 360

Ile Thr Leu Thr Lys Phe Phe Tyr Ala Ile Ser Ser Ser Lys Ser  
365 370 375

Ser Asn Val Ile Val Leu Leu Leu Ala Gln Ile Met Gly Met Tyr  
380 385 390

Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser Met Pro Leu Glu  
395 400 405

Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu Gln Phe Asn

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

410

415

420

Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser Ala Leu  
425 430 435

Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro Glu  
440 445 450

Lys Gln Met Ala Pro  
455

&lt;210&gt; 431

&lt;211&gt; 407

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; 78, 81, 113, 157, 224, 297

&lt;223&gt; unknown base

&lt;400&gt; 431

catgggaagt ggagccggag ccttccttac actcgccatg agtttcctca 50

tcgactccag catcatgatt acctcccnga nactatTTTT tggatttggg 100

tggcttttct tcngcgccaa tgtttaaaga ctatgagata cgtcagtatg 150

ttgtacnggt gatcttctcc gtgacgtttg ccatttcttg caccatgttt 200

gagctcatca tctttgaaat cttnggagta ttgaatagca gctcccgta 250

ttttcactgg aaaatgaacc tgtgtgtaat tctgctgac ctggttntca 300

tgggtgccttt ttacattggc tattttattg tgagcaatat ccgactactg 350

cataaacaac gactgctttt ttctgtctc ttatggctga cctttatgta 400

tttcag 407

&lt;210&gt; 432

&lt;211&gt; 457

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434

&lt;223&gt; unknown base

&lt;400&gt; 432

gtgttgccct tggggagggg aaggggagcc nggcccttc ctaaaatttg 50

gccaaagggtt tcttnttga attccgggtt nngnatacct tcccagaaaa 100

tattttttgg atttgggta gnttttttc atgcgccaat tgtttaaaga 150

ctatgagata cgtcagtatg ttgtacaggt gatntntcc gtgacgtttg 200

cattttcttg caccatgttt gagctcatca tntttgaaat nttaggagta 250  
 ttgaatagca gctcccgtta ttttcaactgg aaaatgaacc tgtgtgtaat 300  
 tctgctgata ctggttttca tgggtgccttt ttacattggc tattttattg 350  
 tgagcaatat ccgactactg cataaacaac gactgctttt ttcctgtctn 400  
 ttatggctga cctttatgta tttnttntgg aaantaggag atccctttcc 450  
 cattctc 457

<210> 433  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 433  
 aagtggagcc ggagccttcc 20

<210> 434  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 434  
 tcgttggtta tgcagtagtc gg 22

<210> 435  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 435  
 attgtttaaa gactatgaga tacgtcagta tgttgtagag g 41

<210> 436  
 <211> 3951  
 <212> DNA  
 <213> Homo sapiens

<400> 436  
 ctgcgcgagg gatcgtccca tggccggggc tcggagccgc gacccttggg 50  
 gggcctccgg gatttgctac ctttttggt cctgctcgt cgaactgctc 100  
 ttctcacggg ctgtcgcctt caatctggac gtgatgggtg ccttgccgaa 150  
 ggagggcgag ccaggcagcc tcttcggctt ctctgtggcc ctgcaccggc 200



tccccgtgtg acgttcctga gccgtaacct ggaagaaccc aagcaccagg 1700  
 cctcgggcac cgtgtggctg aagcaccagc atgaccgagt ctgtggagac 1750  
 gccatgttcc agctecagga aaatgtcaaa gacaagcttc gggccattgt 1800  
 agtgacctg tcctacagtc tccagacccc tcggctccgg cgacaggctc 1850  
 ctggccaggg gctgcctcca gtggccccc tctcaatgc ccaccagccc 1900  
 agcaccacgc gggcagagat ccacttcctg aagcaaggct gtggtgaaga 1950  
 caagatctgc cagagcaatc tgcagctggt ccacgcccgc ttctgtaccc 2000  
 gggtcagcga cacggaattc caacctctgc ccatggatgt ggatggaaca 2050  
 acagccctgt ttgcactgag tgggcagcca gtcattggcc tggagctgat 2100  
 ggtcaccaac ctgccatcgg acccagccca gcccaggct gatggggatg 2150  
 atgccatga agcccagctc ctggctcatgc ttctgactc actgcactac 2200  
 tcaggggtcc gggccctgga ccctgcggag aagccactct gcctgtccaa 2250  
 tgagaatgcc tcccatgttg agtgtgagct ggggaacccc atgaagagag 2300  
 gtgccagggt caccttctac ctcatcctta gcacctccgg gatcagcatt 2350  
 gagaccacgg aactggaggt agagctgctg ttggccacga tcagtgaagca 2400  
 ggagctgcat ccagtctctg cagcagcccg tgtcttcatt gagctgccac 2450  
 tgtccattgc aggaatggcc attccccagc aactcttctt ctctggtgtg 2500  
 gtgaggggag agagagccat gcagtctgag cgggatgtgg gcagcaagg 2550  
 caagtatgag gtcacggttt ccaaccaagg ccagtcgctc agaaccctgg 2600  
 gctctgcctt cctcaacatc atgtggcctc atgagattgc caatgggaag 2650  
 tggttgctgt acccaatgca ggttgagctg gagggcgggc aggggcctgg 2700  
 gcagaaaggg ctttgctctc ccaggcccaa catcctccac ctggatgtgg 2750  
 acagtaggga taggaggcgg cgggagctgg agccacctga gcagcaggag 2800  
 cctggtgagc ggcaggagcc cagcatgtcc tggtagccag tgctctctgc 2850  
 tgagaagaag aaaaacatca ccctggactg cggccggggc acggccaact 2900  
 gtgtggtggt cagctgccca ctctacagct ttgaccgcgc ggctgtgctg 2950  
 catgtctggg gccgtctctg gaacagcacc tttctggagg agtactcagc 3000  
 tgtgaagtcc ctggaagtga ttgtccgggc caacatcaca gtgaagtcct 3050  
 ccataaagaa cttgatgctc cgagatgcct ccacagtgat ccagtgatg 3100





	80		85		90
Leu Phe Ala Cys	Pro Leu Ser Leu Glu	Glu Thr Asp Cys Tyr Arg			
	95	100			105
Val Asp Ile Asp	Gln Gly Ala Asp Met	Gln Lys Glu Ser Lys Glu			
	110	115			120
Asn Gln Trp Leu	Gly Val Ser Val Arg	Ser Gln Gly Pro Gly Gly			
	125	130			135
Lys Ile Val Thr	Cys Ala His Arg Tyr	Glu Ala Arg Gln Arg Val			
	140	145			150
Asp Gln Ile Leu	Glu Thr Arg Asp Met	Ile Gly Arg Cys Phe Val			
	155	160			165
Leu Ser Gln Asp	Leu Ala Ile Arg Asp	Glu Leu Asp Gly Gly Glu			
	170	175			180
Trp Lys Phe Cys	Glu Gly Arg Pro Gln	Gly His Glu Gln Phe Gly			
	185	190			195
Phe Cys Gln Gln	Gly Thr Ala Ala Ala	Phe Ser Pro Asp Ser His			
	200	205			210
Tyr Leu Leu Phe	Gly Ala Pro Gly Thr	Tyr Asn Trp Lys Gly Thr			
	215	220			225
Ala Arg Val Glu	Leu Cys Ala Gln Gly	Ser Ala Asp Leu Ala His			
	230	235			240
Leu Asp Asp Gly	Pro Tyr Glu Ala Gly	Gly Glu Lys Glu Gln Asp			
	245	250			255
Pro Arg Leu Ile	Pro Val Pro Ala Asn	Ser Tyr Phe Gly Phe Ser			
	260	265			270
Ile Asp Ser Gly	Lys Gly Leu Val Arg	Ala Glu Glu Leu Ser Phe			
	275	280			285
Val Ala Gly Ala	Pro Arg Ala Asn His	Lys Gly Ala Val Val Ile			
	290	295			300
Leu Arg Lys Asp	Ser Ala Ser Arg Leu	Val Pro Glu Val Met Leu			
	305	310			315
Ser Gly Glu Arg	Leu Thr Ser Gly Phe	Gly Tyr Ser Leu Ala Val			
	320	325			330
Ala Asp Leu Asn	Ser Asp Gly Trp Pro	Asp Leu Ile Val Gly Ala			
	335	340			345
Pro Tyr Phe Phe	Glu Arg Gln Glu Glu	Leu Gly Gly Ala Val Tyr			
	350	355			360
Val Tyr Leu Asn	Gln Gly Gly His Trp	Ala Gly Ile Ser Pro Leu			
	365	370			375

Arg Leu Cys Gly Ser Pro Asp Ser Met Phe Gly Ile Ser Leu Ala  
380 385 390

Val Leu Gly Asp Leu Asn Gln Asp Gly Phe Pro Asp Ile Ala Val  
395 400 405

Gly Ala Pro Phe Asp Gly Asp Gly Lys Val Phe Ile Tyr His Gly  
410 415 420

Ser Ser Leu Gly Val Val Ala Lys Pro Ser Gln Val Leu Glu Gly  
425 430 435

Glu Ala Val Gly Ile Lys Ser Phe Gly Tyr Ser Leu Ser Gly Ser  
440 445 450

Leu Asp Met Asp Gly Asn Gln Tyr Pro Asp Leu Leu Val Gly Ser  
455 460 465

Leu Ala Asp Thr Ala Val Leu Phe Arg Ala Arg Pro Ile Leu His  
470 475 480

Val Ser His Glu Val Ser Ile Ala Pro Arg Ser Ile Asp Leu Glu  
485 490 495

Gln Pro Asn Cys Ala Gly Gly His Ser Val Cys Val Asp Leu Arg  
500 505 510

Val Cys Phe Ser Tyr Ile Ala Val Pro Ser Ser Tyr Ser Pro Thr  
515 520 525

Val Ala Leu Asp Tyr Val Leu Asp Ala Asp Thr Asp Arg Arg Leu  
530 535 540

Arg Gly Gln Val Pro Arg Val Thr Phe Leu Ser Arg Asn Leu Glu  
545 550 555

Glu Pro Lys His Gln Ala Ser Gly Thr Val Trp Leu Lys His Gln  
560 565 570

His Asp Arg Val Cys Gly Asp Ala Met Phe Gln Leu Gln Glu Asn  
575 580 585

Val Lys Asp Lys Leu Arg Ala Ile Val Val Thr Leu Ser Tyr Ser  
590 595 600

Leu Gln Thr Pro Arg Leu Arg Arg Gln Ala Pro Gly Gln Gly Leu  
605 610 615

Pro Pro Val Ala Pro Ile Leu Asn Ala His Gln Pro Ser Thr Gln  
620 625 630

Arg Ala Glu Ile His Phe Leu Lys Gln Gly Cys Gly Glu Asp Lys  
635 640 645

Ile Cys Gln Ser Asn Leu Gln Leu Val His Ala Arg Phe Cys Thr  
650 655 660

Arg Val Ser Asp Thr Glu Phe Gln Pro Leu Pro Met Asp Val Asp

PROTEIN 1000

				665						670					675
Gly	Thr	Thr	Ala	Leu	Phe	Ala	Leu	Ser	Gly	Gln	Pro	Val	Ile	Gly	
				680					685					690	
Leu	Glu	Leu	Met	Val	Thr	Asn	Leu	Pro	Ser	Asp	Pro	Ala	Gln	Pro	
				695					700					705	
Gln	Ala	Asp	Gly	Asp	Asp	Ala	His	Glu	Ala	Gln	Leu	Leu	Val	Met	
				710					715					720	
Leu	Pro	Asp	Ser	Leu	His	Tyr	Ser	Gly	Val	Arg	Ala	Leu	Asp	Pro	
				725					730					735	
Ala	Glu	Lys	Pro	Leu	Cys	Leu	Ser	Asn	Glu	Asn	Ala	Ser	His	Val	
				740					745					750	
Glu	Cys	Glu	Leu	Gly	Asn	Pro	Met	Lys	Arg	Gly	Ala	Gln	Val	Thr	
				755					760					765	
Phe	Tyr	Leu	Ile	Leu	Ser	Thr	Ser	Gly	Ile	Ser	Ile	Glu	Thr	Thr	
				770					775					780	
Glu	Leu	Glu	Val	Glu	Leu	Leu	Leu	Ala	Thr	Ile	Ser	Glu	Gln	Glu	
				785					790					795	
Leu	His	Pro	Val	Ser	Ala	Arg	Ala	Arg	Val	Phe	Ile	Glu	Leu	Pro	
				800					805					810	
Leu	Ser	Ile	Ala	Gly	Met	Ala	Ile	Pro	Gln	Gln	Leu	Phe	Phe	Ser	
				815					820					825	
Gly	Val	Val	Arg	Gly	Glu	Arg	Ala	Met	Gln	Ser	Glu	Arg	Asp	Val	
				830					835					840	
Gly	Ser	Lys	Val	Lys	Tyr	Glu	Val	Thr	Val	Ser	Asn	Gln	Gly	Gln	
				845					850					855	
Ser	Leu	Arg	Thr	Leu	Gly	Ser	Ala	Phe	Leu	Asn	Ile	Met	Trp	Pro	
				860					865					870	
His	Glu	Ile	Ala	Asn	Gly	Lys	Trp	Leu	Leu	Tyr	Pro	Met	Gln	Val	
				875					880					885	
Glu	Leu	Glu	Gly	Gly	Gln	Gly	Pro	Gly	Gln	Lys	Gly	Leu	Cys	Ser	
				890					895					900	
Pro	Arg	Pro	Asn	Ile	Leu	His	Leu	Asp	Val	Asp	Ser	Arg	Asp	Arg	
				905					910					915	
Arg	Arg	Arg	Glu	Leu	Glu	Pro	Pro	Glu	Gln	Gln	Glu	Pro	Gly	Glu	
				920					925					930	
Arg	Gln	Glu	Pro	Ser	Met	Ser	Trp	Trp	Pro	Val	Ser	Ser	Ala	Glu	
				935					940					945	
Lys	Lys	Lys	Asn	Ile	Thr	Leu	Asp	Cys	Ala	Arg	Gly	Thr	Ala	Asn	
				950					955					960	

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala	965	970	975
Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu	980	985	990
Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn	995	1000	1005
Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala	1010	1015	1020
Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val	1025	1030	1035
Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu	1040	1045	1050
Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys	1055	1060	1065
Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro	1070	1075	1080
Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe	1085	1090	1095
Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser	1100	1105	1110
Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp	1115	1120	1125
Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr	1130	1135	1140

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgtctc tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439  
gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

cgcgccgggc gcaggagct gaggggacgg ctcgagacgg cggcgcgtgc 50

agcagctcca gaaagcagcg agttggcaga gcagggctgc atttccagca 100

ggagctgcga gcacagtgtt ggctcacaac aagatgtctc aggtgtcagc 150

cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcagctg 200

ccgcggcggg ggctgcagcc ggggggcggg cggacggcgg taattttctg 250

gatgataaac aatggctcac cacaatctct cagtatgaca aggaagtcgg 300

acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350

ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400

tgcttaaaga tgaaatgtag tgcacataaa gtatgcattg ctcaagattc 450

tcagactgca gtctgcatta gtcaccggag gcttacacac aggatgaaag 500

aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550

aagcagtgcc cagtgtctta tcccagccct gtttgtggtt cagatggtca 600

tacctactct ttccagtgc aactagaata tcaggcatgt gtcttaggaa 650

aacagatctc agtcaaatgt gaaggacatt gcccatgtcc ttcagataag 700

cccaccagta caagcagaaa tgtaagaga gcatgcagt acctggagtt 750

caggggaagt gcaaacagat tgcgggactg gttcaaggcc cttcatgaaa 800

gtggaagtca aaacaagaag acaaaaacat tgctgaggcc tgagagaagc 850

agattcgata ccagcatctt gccaatgtgc aaggactcac ttggctggat 900

gtttaacaga cttgatacaa actatgacct gctattggac cagtcagagc 950

1000 1050 1100 1150 1200 1250 1300 1350 1400 1450 1500 1550 1600 1650 1700 1750 1800 1850 1900 1950

tcagaagcat ttaccttgat aagaatgaac agtgtaccaa ggcattcttc 1000  
aattcttggtg acacatacaa ggacagttta atatctaata atgagtgggtg 1050  
ctactgcttc cagagacagc aagacccacc ttgccagact gagctcagca 1100  
atattcagaa gcggcaaggg gtaaagaagc tcctaggaca gtatatcccc 1150  
ctgtgtgatg aagatgggta ctacaagcca acacaatgtc atggcagtgt 1200  
tggacagtgc tgggtgtgtg acagatatgg aatgaagtc atgggatcca 1250  
gaataaatgg tgttcagat tgtgctatag attttgagat ctccggagat 1300  
tttgctagtg gcgattttca tgaatggact gatgatgagg atgatgaaga 1350  
cgatattatg aatgatgaag atgaaattga agatgatgat gaagatgaag 1400  
gggatgatga tgatgggtgt gatgaccatg atgtatacat ttgattgatg 1450  
acagttgaaa tcaataaatt ctacatttct aatatttaca aaaatgatag 1500  
cctattttaa attatcttct tccccataa caaatgatt ctaaactca 1550  
catatatatt gtataattat ttgaaaaatt gcagctaaag ttatagaact 1600  
ttatgtttaa ataagaatca tttgctttga gtttttatat tccttacaca 1650  
aaaagaaaat acatatgcag tctagtcaga caaaataaag ttttgaagtg 1700  
ctactataat aaatttttca cgagaacaaa ctttgtaaatt cttccataag 1750  
caaatgaca gctagtgtt gggatcgtac atgttaattt tttgaaagat 1800  
aattctaagt gaaattttaa ataaataaat ttttaatgac ctgggtctta 1850  
aggatttagg aaaaatatgc atgctttaat tgcatttcca aagtagcatc 1900  
ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950  
aaaaaaaaaaaa 1964

<210> 442  
<211> 436  
<212> PRT  
<213> Homo sapiens

<400> 442  
Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Trp  
1 5 10 15  
Cys Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly  
20 25 30  
Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu  
35 40 45  
Thr Thr Ile Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys

60

Lys Lys Leu Leu Gly Gln Tyr Ile Pro Leu Cys Asp Glu Asp Gly  
 . 335 340 345

308



Tyr Tyr Lys Pro Thr Gln Cys His Gly Ser Val Gly Gln Cys Trp  
 350 355 360  
 Cys Val Asp Arg Tyr Gly Asn Glu Val Met Gly Ser Arg Ile Asn  
 365 370 375  
 Gly Val Ala Asp Cys Ala Ile Asp Phe Glu Ile Ser Gly Asp Phe  
 380 385 390  
 Ala Ser Gly Asp Phe His Glu Trp Thr Asp Asp Glu Asp Asp Glu  
 395 400 405  
 Asp Asp Ile Met Asn Asp Glu Asp Glu Ile Glu Asp Asp Asp Glu  
 410 415 420  
 Asp Glu Gly Asp Asp Asp Asp Gly Gly Asp Asp His Asp Val Tyr  
 425 430 435

Ile

<210> 443  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic oligonucleotide probe  
 <400> 443  
 cagcaatatt cagaagcggc aaggg 25  
 <210> 444  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic oligonucleotide probe  
 <400> 444  
 catcatggtc atcaccacca tcatcatc 28  
 <210> 445  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic oligonucleotide probe  
 <400> 445  
 ggttactaca agccaacaca atgtcatggc agtgttggac agtgctgg 48  
 <210> 446  
 <211> 3617  
 <212> DNA  
 <213> Homo sapiens

<400> 446

cagactccag atttccctgt caaccacgag gaggccagag aggaaacgcg 50  
gagcggagac aacagtacct gacgcctctt tcagcccggg atcgccccag 100  
cagggatggg cgacaagatc tggtgacct tccccgtgt cttctggcc 150  
gctctgcctc cgggtgctgt gctggggcg gccggcttca caccttcct 200  
cgatagcgac ttcaccttta ccctcccg cggccagaag gaggcttct 250  
accagcccat gccctgaag gctcgctgg agatcgagta ccaagtttta 300  
gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350  
aaccttagtt tttgaacaaa gaaaatcaga tggagttcac actgtagaga 400  
ctgaagttgg tgattacatg ttctgcttg acaatacatt cagcaccatt 450  
tctgagaagg tgattttctt tgaattaatc ctggataata tgggagaaca 500  
ggcacaagaa caagaagatt ggaagaaata tattactggc acagatatat 550  
tggatatgaa actggaagac atcctggaat ccatcaacag catcaagtcc 600  
agactaagca aaagtgggca catacaaatt ctgcttagag catttgaagc 650  
tcgtgatcga aacatacaag aaagcaactt tgatagagtc aatttctggt 700  
ctatggttaa tttagtggtc atggtggtg tgtcagccat tcaagtttat 750  
atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaactc 800  
caaactagag tacgtaacat tgaaaaatga ggcataaaaa tgcaataaac 850  
tgttacagtc aagaccatta atggtcttct ccaaaatatt ttgagatata 900  
aaagtaggaa acaggtataa ttttaatgtg aaaattaagt cttcactttc 950  
tgtgcaagta atcctgctga tccagttgta cttaagtgtg taacaggaat 1000  
attttgcaga atataggttt aactgaatga agccatatta ataactgcat 1050  
tttccctaact ttgaaaaatt ttgcaaatgt cttaggtgat ttaaataaat 1100  
gagtattggg cctaattgca acaccagtct gtttttaaca ggttctatta 1150  
cccagaactt ttttgtaaat gcggcagtta caaattaact gtggaagttt 1200  
tcagttttta gttataaatc acctgagaat tacctaataga tggattgaat 1250  
aaatctttag actacaaaag cccaactttt ctctatttac atatgcatct 1300  
ctcctataat gtaaatagaa taatagcttt gaaatacaat taggtttttg 1350  
agatttttat aaccaaatac atttcagtgt aacatattag cagaaagcat 1400  
tagtctttgt actttgctta cattcccaa agctgacatt ttcacgattc 1450

ttaaaaacac aaagttacac ttactaaaat taggacatgt tttctctttg 1500  
 aaatgaagaa tatagtttaa aagcttcctc ctccataggg acacattttc 1550  
 tctaaccctt aactaaagt taggatttta aaattaaatg tgaggtaaaa 1600  
 taagtttatt tttaatagta tctgtcaagt taatatctgt caacagttaa 1650  
 taatcatggt atgttaattt taacatgatt gctgacttgg ataattcatt 1700  
 attaccagca gttatgaagg aaatattgct aaaatgatct gggcctacca 1750  
 taaataaata tctccttttc tgagctctaa gaattatcag aaaacaggaa 1800  
 agaatttaga aaaacttgag aaaacctaatt ccaaaataaa attcacttaa 1850  
 gtagaactat aaataaatat ctagaatctg actggctcat catgacatcc 1900  
 tactcataac ataaatcaaa ggagatgatt aatttccagt tagctggaag 1950  
 aaactttggc tgtaggtttt tttttctac aagaattctg gtttgaatta 2000  
 tttttgtaag caggtacatt ttataaaatg taagccctac tgtaaggttt 2050  
 agcactgggt gtacatattt attaaaaatt tttattataa caacttttat 2100  
 taaaatggcc tttctgaaca ctttatttat tgatgttgaa gtaaggatta 2150  
 gaaacataga ctccaagtt ttaaaccact aaatgtgaat aacctatata 2200  
 tacaacaaag tttctgccat ctactttttt gaagtctatg ggggtcttac 2250  
 tcaagtacta gtaatttaac ttcacatga atgaactata atttttaagt 2300  
 tatgccatt tataacggtt tttatgacta cattgtgagt tagaaacaaa 2350  
 cttaaaattt ggggtataga acccctcaac aggttagtaa tgctggaatt 2400  
 cttgatgagc aataatgata accagagagt gatttcattt acactcatag 2450  
 tagtataaaa agagatacat ttccctctta ggcccctggg agaagagcag 2500  
 cttagatttc cctactggca aggtttttta aaatgaggta aatgccgtat 2550  
 atgatcaatt accttaattg gccaagaaaa tgcttcaggt gtctaggggt 2600  
 atcctctgca acacttgag aacaaaggtc aataagatcc ttgcctatga 2650  
 ataccctcc cttttgcgct gttaaatttg caatgagaag caaatttaca 2700  
 gtaccataac taataaagca gggtagagat ataaactact gcatcttttc 2750  
 tataaaactg tgattaagaa ttctacctct cctgtatggc tgttactgta 2800  
 ctgtactctc tgactcctta cctaacaatg aatttggtac ataactttct 2850  
 acatgtatga tttgtgccac tgatcttaaa cctatgattc agtaacttct 2900

TOPIC: H3C4FOOT

taccatataa aaacgataat tgctttatct ggaaaagaat ttaggaatac 2950  
 taaggacaat tatttttata gacaaagtaa aaagacagat atttaagagg 3000  
 cataaccaa aaagcaaaac ttgtaaacag agtaaaaatc tttaatatct 3050  
 ctaaagacat actgtttatc tgcttcatat gcttttttta atttcactat 3100  
 tccatttcta aattaaagtt atgctaaatt gagtaagctg tttatcactt 3150  
 aacagctcat tttgtctttt tcaatataca aattttaaaa atactacaat 3200  
 atttaactaa ggccaacccg atttcataa tgtagcagtt accgtgttca 3250  
 cctcacacta aggccatagag ttgtctctga tatgcatttg gatgattaat 3300  
 gttatgctgt tctttcatgt gaatgtcaag acatggaggg tgtttgtaat 3350  
 tttatggtaa aattaatcct tcttacacat aatgggtgtc taaaattgac 3400  
 aaaaaatgag cacttacaat tgtatgtctc ctcaaatgaa gattctttat 3450  
 gtgaaatttt aaaagacatt gattccgcat gtaaggattt ttcactgaa 3500  
 gtacaataat gcacaatcag tgttgctcaa actgctttat acttataaac 3550  
 agccatctta aataagcaac gtattgtgag tactgatatg tatataataa 3600  
 aaattatcaa aggaaaa 3617

<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

Met	Gly	Asp	Lys	Ile	Trp	Leu	Pro	Phe	Pro	Val	Leu	Leu	Leu	Ala
1				5					10					15

Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30

Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45

Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60

Glu	Tyr	Gln	Val	Leu	Asp	Gly	Ala	Gly	Leu	Asp	Ile	Asp	Phe	His
				65					70					75

Leu	Ala	Ser	Pro	Glu	Gly	Lys	Thr	Leu	Val	Phe	Glu	Gln	Arg	Lys
				80					85					90

Ser	Asp	Gly	Val	His	Thr	Val	Glu	Thr	Glu	Val	Gly	Asp	Tyr	Met
				95					100					105

Phe	Cys	Phe	Asp	Asn	Thr	Phe	Ser	Thr	Ile	Ser	Glu	Lys	Val	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

110 115 120  
 Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu  
 125 130 135  
 Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp  
 140 145 150  
 Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser  
 155 160 165  
 Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe  
 170 175 180  
 Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val  
 185 190 195  
 Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser  
 200 205 210  
 Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg  
 215 220 225

Lys Ser Arg Thr

<210> 448

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

cccagcaggg ctgggcgaca aga 23

<210> 449

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

gtcttcaggt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccagaaggag cacggggaag ggcagccaga tctgtcgcc cat 43

<210> 451  
 <211> 859  
 <212> DNA  
 <213> Homo sapiens

<400> 451  
 ccatccctga gatcttttta taaaaaaccc agtctttgct gaccagacaa 50  
 agcataccag atctcaccag agagtcgcag acactatgct gcctcccatg 100  
 gccctgccca gtgtgtcctg gatgtgtgtt tcctgcctca ttctcctgtg 150  
 tcaggttcaa ggtgaagaaa cccagaagga actgccctct ccacggatca 200  
 gctgtcccaa aggctccaag gcctatggct cccoctgcta tgccttgttt 250  
 ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300  
 ctctggaaaa ctggtgtctg tgctcagtgg ggctgaggga tccttcgtgt 350  
 cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400  
 ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450  
 gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500  
 ccatcttaaa ccctggccac tgtgggagcc tgtcaagaag cacaggattt 550  
 ctgaagtgga aagattataa ctgtgatgca aagttaccct atgtctgcaa 600  
 gttcaaggac tagggcaggt ggaagtacag cagcctcagc ttggcgtgca 650  
 gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700  
 ttctcccaa actgccctac ctgactacct tgtcatgac ctccttcttt 750  
 ttctttttt ttacacttca tttcaggctt ttctgtgtt tccatgtctt 800  
 gagatctcag agaataataa taaaatggt actttataaa aaaaaaaaaa 850  
 aaaaaaaaaa 859

<210> 452  
 <211> 175  
 <212> PRT  
 <213> Homo sapiens

<400> 452  
 Met Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu  
 1 5 10 15  
 Ser Cys Leu Ile Leu Leu Cys Gln Val Gln Gly Glu Glu Thr Gln  
 20 25 30  
 Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys  
 35 40 45  
 Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser



<400> 454

Met Arg Gly Thr Arg Leu Ala Leu Leu Ala Leu Val Leu Ala Ala  
1 5 10 15

Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu  
20 25 30

Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr  
35 40 45

Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val  
50 55 60

Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser  
65 70 75

Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro  
80 85 90

Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro  
95 100 105

Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu  
110 115 120

Leu Ser Leu Arg Leu  
125

<210> 455

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 455

ctgcagtcag gactctggga ccgcaggggg ctccccggacc ctgactctgc 50

agccgaaccg gcacggtttc gtggggaccc aggcttgcaa agtgacggtc 100

attttctctt tctttctccc tcttgagtcc ttctgagatg atggctcttg 150

gcgcagcggg agctaccgag gtctttgtcg cgatggtagc ggcggctctc 200

ggcggccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250

ttccaacgct atcaagaacc tgccccacc gctgggcggc gctgcggggc 300

accaggtc tgcaagcagc gccgcgccg gaatcctgta cccgggagg 350

aataagtacc agaccattga caactaccag ccgtaccggt gcgcagagga 400

cgaggagtgc ggcactgatg agtactgagc tagtcccacc cgcgaggagg 450

acgcaggcgt gcaaatctgt ctgcctgca ggaagcgccg aaaacgctgc 500

atgcgtcacg ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550

tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600



ctgaaagctt tggtaatgat catagcacct tggatgggta ttccagaaga 650  
 accaccttgt cttcaaaaat gtatcacacc aaaggacaag aaggttctgt 700  
 ttgtctccgg tcatcagact gtgcctcagg attgtgtgt gctagacact 750  
 tctgggtccaa gatctgtaaa cctgtcctga aagaaggta agtgtgtacc 800  
 aagcatagga gaaaaggctc tcatggacta gaaatattcc agcgttggtta 850  
 ctgtggagaa ggtctgtctt gccggataca gaaagatcac catcaagcca 900  
 gtaattcttc taggcttcac acttgtcaga gacactaac cagctatcca 950  
 aatgcagtga actcctttta tataatagat gctatgaaa ccttttatga 1000  
 ccttcatcaa ctcaatccta aggatataca agttctgtgg tttcagttaa 1050  
 gcattccaat aacaccttcc aaaaacctgg agtgtaagag ctttgtttct 1100  
 ttatggaact cccctgtgat tgcagtaaata tactgtattg taaattctca 1150  
 gtgtggcact tacctgtaaa tgcaatgaaa cttttaatta tttttctaaa 1200  
 ggtgctgcac tgcctatttt tcctcttgtt atgtaaattt ttgtacacat 1250  
 tgattgttat ctgactgac aaataattcta tattgaactg aagtaaatca 1300  
 tttcagctta tagttcttaa aagcataacc ctttacccca ttttaattcta 1350  
 gagtctagaa cgcaaggatc tcttggaaatg acaaatgata ggtacctaaa 1400  
 atgtaacatg aaaatactag cttattttct gaaatgtact atcttaatgc 1450  
 ttaaattata tttcccttta ggctgtgata gtttttgaaa taaaatttaa 1500  
 catttaaaaa aaaaaaaaa 1518

<210> 456  
 <211> 266  
 <212> PRT  
 <213> Homo sapiens

<400> 456  
 Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala  
 1 5 10 15  
 Met Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser  
 20 25 30  
 Ala Thr Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu  
 35 40 45  
 Pro Pro Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val  
 50 55 60  
 Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln  
 65 70 75



```
<210> 458
<211> 4040
<212> DNA
<213> Homo sapiens
```

319

ttgttaaatt ttactcccc aggtgttca cactgcatg atttagctcc 900  
 cacatggaga gactttgcta aagaagtga tgggttactt cgaattggag 950  
 ctgttaactg tggatgat agaatgttt gccgaatgaa aggagtcaac 1000  
 agctatccca gtctcttcat ttttcgtct ggaatggccc cagtgaata 1050  
 tcatggagac agatcaaagg agagttagt gagttttgca atgcagcatg 1100  
 ttagaagtac agtgacagaa ctttgacag gaaattttgt caactccata 1150  
 caaactgctt ttgtctgtgg tattggctgg ctgatcactt ttgttcaaa 1200  
 aggaggagat tgtttgactt cacagacacg actcaggctt agtggcatgt 1250  
 tgtttctcaa ctattggat gctaaagaaa tatatttga agtaatacat 1300  
 aatcttcag atttgaact acttcggca aacacactag aggtcgttt 1350  
 ggctcatcat cgttggtgt tatttttca ttttgaaaa aatgaaatt 1400  
 caaatgatcc tgagctgaaa aaactaaaa ctctacttaaatgatcat 1450  
 attcaagttg gcaggtttga ctgttctct gcaccagaca tctgtagtaa 1500  
 tctgtatgtt tttcagcgt ctctagcagt atttaaagga caaggaacca 1550  
 aagaatatga aattcatcat ggaagaaga ttctatatga tataactgcc 1600  
 tttgcaaaag aaagtgtgaa ttctcatgtt accacgcttg gacctcaaaa 1650  
 ttttctgcc aatgacaaag aacctggct tgttgatttc tttgcccct 1700  
 ggtgtccacc atgtcgagct ttactaccag agttacgaag agcatcaaatt 1750  
 cttctttatg gtcagcttaa gtttggtaca ctagattgta cagttcatga 1800  
 gggactctgt aacatgtata acattcagc ttatccaaca acagtggat 1850  
 tcaaccagtc caacattcat gagtatgaag gacatcactc tgctgaacaa 1900  
 atcttgagat tcatagagga tcttatgaat cttcagtggt tctcccttac 1950  
 acccaccacc ttcaacgaac tagttacaca aagaaacac aacgaagtct 2000  
 ggatggttga tttctattct ccgtggtgtc atccttgcca agtcttaattg 2050  
 ccagaatgga aaagaatggc ccggacatta actggactga tcaacgtggg 2100  
 cagtatagat tgccaacagt atcattcttt ttgtgccag gaaaacgttc 2150  
 aaagataccc tgagataaga ttttttcccc caaatcaaa taaagcttat 2200  
 cagtatcaca gttacaatgg ttggaatagg gatgcttatt ccctgagaat 2250  
 ctggggtcta ggatttttac ctcaagtatc cacagatcta acacctcaga 2300

ctttcagtga aaaagttcta caagggaaaa atcattgggt gattgatttc 2350  
tatgctcctt ggtgtggacc ttgccagaat tttgctccag aatttgagct 2400  
cttggttagg atgattaaag gaaaagtga agctggaaaa gtagactgtc 2450  
aggcttatgc tcagacatgc cagaaagctg ggatcagggc ctatccaact 2500  
gttaagtttt atttctacga aagagcaaag agaaattttc aagaagagca 2550  
gataaatacc agagatgcaa aagcaatcgc tgccttaata agtgaaaaat 2600  
tggaactct ccgaaatcaa ggcaagagga ataaggatga actttgataa 2650  
tgttgaagat gaagaaaaag tttaaaagaa attctgacag atgacatcag 2700  
aagacaccta tttagaatgt tacatttatg atgggaatga atgaacatta 2750  
tcttagactt gcagttgtac tgccagaatt atctacagca ctggtgtaaa 2800  
agaagggtct gcaaactttt tctgtaaagg gccggtttat aaatatttta 2850  
gactttgcag gctataatat atggttcaca catgagaaca agaataagat 2900  
catcatgtat tctttgttat ttgcttttaa caaccttaa aaaatattaa 2950  
aacgattctt agctcagagc catacaaaaag taggctggat tcagtccatg 3000  
gaccatagat tgctgtcccc ctgcacggac ttataatggt tcagggtggct 3050  
ggcttgaaca tgagtctgct gtgctatcta cataaatgtc taagttgtat 3100  
aaagtccact ttcccttcac gttttttggc tgacctgaaa agaggttaact 3150  
tagtttttgg tcacttgctt tcctaaaaat gctatcccta accatatatt 3200  
tatatttcgt tttaaaaaca cccatgatgt ggcacagtaa acaaacctg 3250  
ttatgctgta ttattatgag gagattcttc attgttttct ttccttctca 3300  
aaggttgaaa aaatgctttt aatttttcac agccgagaaa cagtgcagca 3350  
gtatatgtgc acacagtaag tacacaaatt tgagcaacag taagtgcaca 3400  
aattctgtag tttgctgtat catccaggaa aacctgaggg aaaaaatta 3450  
tagcaattaa ctgggcattg tagagtatcc taaatatggt atcaagtatt 3500  
tagagttcta tattttaaag atatatgtgt tcatgtattt tctgaaattg 3550  
ctttcataga aattttccca ctgatagtgt atttttgagg catctaatat 3600  
ttacatattt gccttctgaa ctttgttttg acctgtatcc tttatttaca 3650  
ttgggttttt ctttcatagt tttggttttt cactcctgtc cagtctattt 3700  
attattcaaa taggaaaaat tactttacag gttgttttac tgtagcttat 3750

aatgatactg tagttattcc agttactagt ttactgtcag agggctgcct 3800  
 ttttcagata aatattgaca taataactga agttatTTTT ataagaaaat 3850  
 caagtatata aatctaggaa agggatcttc tagtttctgt gttgtttaga 3900  
 ctcaaagaat cacaaatttg tcagtaacat gtagttgttt agttataatt 3950  
 cagagtgtac agaatggtaa aaattccaat cagtcaaaag aggtcaatga 4000  
 attaaaaggc ttgcaacttt ttcaaaaaaa aaaaaaaa 4040

<210> 459  
 <211> 747  
 <212> PRT  
 <213> Homo sapiens

<400> 459

Met	Gly	Val	Trp	Leu	Asn	Lys	Asp	Asp	Tyr	Ile	Arg	Asp	Leu	Lys	1	5	10	15
Arg	Ile	Ile	Leu	Cys	Phe	Leu	Ile	Val	Tyr	Met	Ala	Ile	Leu	Val	20	25	30	
Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr	35	40	45	
Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu	50	55	60	
Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly	65	70	75	
Asp	Phe	Leu	Lys	Ile	Asn	Arg	Ala	Tyr	Glu	Val	Leu	Lys	Asp	Glu	80	85	90	
Asp	Leu	Arg	Lys	Lys	Tyr	Asp	Lys	Tyr	Gly	Glu	Lys	Gly	Leu	Glu	95	100	105	
Asp	Asn	Gln	Gly	Gly	Gln	Tyr	Glu	Ser	Trp	Asn	Tyr	Tyr	Arg	Tyr	110	115	120	
Asp	Phe	Gly	Ile	Tyr	Asp	Asp	Asp	Pro	Glu	Ile	Ile	Thr	Leu	Glu	125	130	135	
Arg	Arg	Glu	Phe	Asp	Ala	Ala	Val	Asn	Ser	Gly	Glu	Leu	Trp	Phe	140	145	150	
Val	Asn	Phe	Tyr	Ser	Pro	Gly	Cys	Ser	His	Cys	His	Asp	Leu	Ala	155	160	165	
Pro	Thr	Trp	Arg	Asp	Phe	Ala	Lys	Glu	Val	Asp	Gly	Leu	Leu	Arg	170	175	180	
Ile	Gly	Ala	Val	Asn	Cys	Gly	Asp	Asp	Arg	Met	Leu	Cys	Arg	Met	185	190	195	
Lys	Gly	Val	Asn	Ser	Tyr	Pro	Ser	Leu	Phe	Ile	Phe	Arg	Ser	Gly				

200	205	210
Met Ala Pro Val Lys Tyr His Gly Asp	Arg Ser Lys Glu Ser Leu	
215	220	225
Val Ser Phe Ala Met Gln His Val Arg	Ser Thr Val Thr Glu Leu	
230	235	240
Trp Thr Gly Asn Phe Val Asn Ser Ile	Gln Thr Ala Phe Ala Ala	
245	250	255
Gly Ile Gly Trp Leu Ile Thr Phe Cys	Ser Lys Gly Gly Asp Cys	
260	265	270
Leu Thr Ser Gln Thr Arg Leu Arg Leu	Ser Gly Met Leu Phe Leu	
275	280	285
Asn Ser Leu Asp Ala Lys Glu Ile Tyr	Leu Glu Val Ile His Asn	
290	295	300
Leu Pro Asp Phe Glu Leu Leu Ser Ala	Asn Thr Leu Glu Asp Arg	
305	310	315
Leu Ala His His Arg Trp Leu Leu Phe	Phe His Phe Gly Lys Asn	
320	325	330
Glu Asn Ser Asn Asp Pro Glu Leu Lys	Lys Leu Lys Thr Leu Leu	
335	340	345
Lys Asn Asp His Ile Gln Val Gly Arg	Phe Asp Cys Ser Ser Ala	
350	355	360
Pro Asp Ile Cys Ser Asn Leu Tyr Val	Phe Gln Pro Ser Leu Ala	
365	370	375
Val Phe Lys Gly Gln Gly Thr Lys Glu	Tyr Glu Ile His His Gly	
380	385	390
Lys Lys Ile Leu Tyr Asp Ile Leu Ala	Phe Ala Lys Glu Ser Val	
395	400	405
Asn Ser His Val Thr Thr Leu Gly Pro	Gln Asn Phe Pro Ala Asn	
410	415	420
Asp Lys Glu Pro Trp Leu Val Asp Phe	Phe Ala Pro Trp Cys Pro	
425	430	435
Pro Cys Arg Ala Leu Leu Pro Glu Leu	Arg Arg Ala Ser Asn Leu	
440	445	450
Leu Tyr Gly Gln Leu Lys Phe Gly Thr	Leu Asp Cys Thr Val His	
455	460	465
Glu Gly Leu Cys Asn Met Tyr Asn Ile	Gln Ala Tyr Pro Thr Thr	
470	475	480
Val Val Phe Asn Gln Ser Asn Ile His	Glu Tyr Glu Gly His His	
485	490	495





<400> 460  
actccccagg ctgttcacac tgcc 24

<210> 461  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 461  
gatcagccag ccaataccag cagc 24

<210> 462  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 462  
gtggtgatga tagaatgctt tgccgaatga aaggagtcaa cagctatccc 50

<210> 463  
<211> 1818  
<212> DNA  
<213> Homo sapiens

<400> 463  
agacagtacc tcctccctag gactacacaa ggactgaacc agaaggaaga 50  
ggacagagca aagccatgaa catcatccta gaaatccttc tgcttctgat 100  
caccatcatc tactcctact tggagtcggt ggtgaagttt ttcatctctc 150  
agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200  
catggaatag gcaggcagac tacttatgaa ttgcaaaac gacagagcat 250  
attggttctg tgggatatta ataagcgcgg tgtggaggaa actgcagctg 300  
agtgccgaaa actaggcgtc actgcgcagc cgtatgtggt agactgcagc 350  
aacagagaag agatctatcg ctctctaaat caggtgaaga aagaagtggg 400  
tgatgtaaca atcgtggtga ataatgctgg gacagtatat ccagccgac 450  
ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 500  
ctaggacatt tttggtacac aaaagcactt cttccatcga tgatggagag 550  
aaatcatggc cacatcgta cagtggcttc agtgtgcggc cacgaaggga 600  
ttcttacct catccatat tgtccagca aatttgccgc tgttggtttt 650  
cacagaggtc tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa 700

aacctcatgt	ctctgccag	tttttgtag	tactgggttc	accaaaaatc	750
caagcacaag	attatggcct	gtattggaga	cagatgaagt	cgtaagaagt	800
ctgatagatg	gaatacttac	caataagaaa	atgatttttg	ttccatcgta	850
tatcaatatc	tttctgagac	tacagaagtt	tcttcctgaa	cgcgccctcag	900
cgatttttaa	tcgtatgcag	aatattcaat	ttgaagcagt	ggttggccac	950
aaaatcaaaa	tgaaatgaat	aaataagctc	cagccagaga	tgtatgcatg	1000
ataatgatat	gaatagtttc	gaatcaatgc	tgcaaagctt	tatttcacat	1050
tttttcagtc	ctgataatat	taaaaacatt	ggtttggcac	tagcagcagt	1100
caaacgaaca	agattaatta	cctgtcttcc	tgtttctcaa	gaatatttac	1150
gtagtttttc	ataggtctgt	ttttcctttc	atgcctctta	aaaacttctg	1200
tgcttacata	aacatactta	aaagggtttc	tttaagatat	tttatttttc	1250
catttaaagg	tggacaaaag	ctacctccct	aaaagtaa	acaaagagaa	1300
cttattttaca	caggggaagg	ttaagactgt	tcaagtagca	ttccaatctg	1350
tagccatgcc	acagaatatc	aacaagaaca	cagaatgagt	gcacagctaa	1400
gagatcaagt	ttcagcaggc	agctttatct	caacctggac	atatttttaag	1450
attcagcatt	tgaaagattt	ccctagcctc	ttcctttttc	attagcccaa	1500
aacgggtgcaa	ctctattctg	gactttatta	cttgattctg	tcttctgtat	1550
aactctgaag	tccaccaaaa	gtggaccctc	tatatcttct	ccctttttat	1600
agtcttataa	gatacattat	gaaagggtgac	cgactctatt	ttaaattctca	1650
gaatttttaag	ttctagcccc	atgataacct	ttttctttgt	aatttatgct	1700
ttcatatatc	cttggtccca	gagatgttta	gacaatttta	ggctcaaaaa	1750
ttaaagctaa	cacaggaaaa	ggaactgtac	tggtctattac	ataagaaaca	1800
atggacccaa	gagaagaa	1818			

<210> 464

<211> 300

<212> PRT

<213> Homo sapiens

$\langle 400 \rangle$  464

Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Leu Ile Thr Ile Ile  
1 5 10 15

Tyr Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg  
20 25 30



<400> 465

cggcggcggc tgcgggcgcg aggtgagggg cgcgaggtga ggggcgcgag 50  
gttcccagca ggatgccccg gctctgcagg aagctgaagt gagaggcccc 100  
gagaggggccc agcccgcccc gggcaggatg accaaggccc ggctgttccg 150  
gctgtggctg gtgtgggggt cgggtgtcat gatcctgctg atcatcgtgt 200  
actgggacag cgcaggcgcc gcgcacttct acttgcacac gtccttctct 250  
aggccgcaca cggggccgcc gctgcccacg cccgggcccg acagggacag 300  
ggagctcacg gccgactccg atgtcgacga gtttctggac aagtttctca 350  
gtgtggcgt gaagcagagc gaccttccca gaaaggagac ggagcagccg 400  
cctgcgccgg ggagcatgga ggagagcgtg agaggctacg actggtcccc 450  
gcgcgacgcc cggcgagcc cagaccaggg ccggcagcag gcggagcgga 500  
ggagcgtgct gcggggcttc tgcgccaact ccagcctggc cttccccacc 550  
aaggagcgcg cattcgacga catccccaac tcggagctga gccacctgat 600  
cgtggacgac cggcacgggg ccatctactg ctacgtgccc aaggtggcct 650  
gcaccaactg gaagcgcgtg atgatcgtgc tgagcggaag cctgctgcac 700  
cgcggtgcdc cctaccgca cccgctgcdc atcccgcgcg agcacgtgca 750  
caacgccagc gcgcacctga ccttcaaaa gttctggcgc cgctacggga 800  
agctctcccc ccacctcatg aaggtcaagc tcaagaagta caccaagttc 850  
ctcttcgtgc gcgaccctt cgtgcgcctg atctccgcct tccgcagcaa 900  
gttcgagctg gagaacgagg agttctaccg caagttcgcc gtgcccacgc 950  
tgcggctgta cgccaaccac accagcctgc ccgcctcggc gcgcgaggcc 1000  
ttccgcgtg gcctcaaggt gtccttcgcc aacttcatcc agtacctgct 1050  
ggaccgcac acggagaagc tggcgccctt caacgagcac tggcggcagg 1100  
tgtaccgcct ctgccaccgc tgccagatcg actacgactt cgtggggaag 1150  
ctggagactc tggacgagga cgccgcgcag ctgctgcagc tactccaggt 1200  
ggaccggcag ctccgcttcc ccccgagcta ccggaacagg accgccagca 1250  
gctgggagga ggactggttc gccaaagatcc ccctggcctg gaggcagcag 1300  
ctgtataaac tctacgaggc cgactttggt ctcttcggct accccaagcc 1350  
cgaaaacctc ctccgagact gaaagcttcc gcgttgcttt ttctcgcgtg 1400  
cctggaacct gacgcacgcg cactccagtt tttttatgac ctacgatttt 1450

atcgatattg tttttaaga ttaatatatt tcaggtattt aatacga 1547

<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

Met Thr Lys Ala Arg Leu Phe Arg Leu Trp Leu Val Leu Gly Ser  
1 5 10 15

Val Phe Met Ile Leu Leu Ile Ile Val Tyr Trp Asp Ser Ala Gly  
20 25 30

Ala Ala His Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr  
35 40 45

Gly Pro Pro Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu  
50 55 60

Thr Ala Asp Ser Asp Val Asp Glu Phe Leu Asp Lys Phe Leu Ser  
65 70 75

Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu Gln  
80 85 90

Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp  
95 100 105

Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln  
110 115 120

Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser  
125 130 135

Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro  
140 145 150

Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala  
155 160 165

Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg  
170 175 180

Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro  
185 190 195

Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala  
200 205 210

Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys  
215 220 225

Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys  
230 235 240

Phe Leu Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala Phe  
 245 250 255  
 Arg Ser Lys Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe  
 260 265 270  
 Ala Val Pro Met Leu Arg Leu Tyr Ala Asn His Thr Ser Leu Pro  
 275 280 285  
 Ala Ser Ala Arg Glu Ala Phe Arg Ala Gly Leu Lys Val Ser Phe  
 290 295 300  
 Ala Asn Phe Ile Gln Tyr Leu Leu Asp Pro His Thr Glu Lys Leu  
 305 310 315  
 Ala Pro Phe Asn Glu His Trp Arg Gln Val Tyr Arg Leu Cys His  
 320 325 330  
 Pro Cys Gln Ile Asp Tyr Asp Phe Val Gly Lys Leu Glu Thr Leu  
 335 340 345  
 Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu Gln Val Asp Arg  
 350 355 360  
 Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn Arg Thr Ala Ser Ser  
 365 370 375  
 Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu Ala Trp Arg Gln  
 380 385 390  
 Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu Phe Gly Tyr  
 395 400 405  
 Pro Lys Pro Glu Asn Leu Leu Arg Asp  
 410

<210> 467  
 <211> 1071  
 <212> DNA  
 <213> Homo sapiens

<400> 467  
 tcgggccaga attcggcacg aggcggcacg agggcgacgg cctcacgggg 50  
 ctttgagagt gaaagaggcc cagagtagag agagagagag accgacgtac 100  
 acgggatggc tacgggaacg cgctatgccg ggaaggtggt ggtcgtgacc 150  
 gggggcgggc gcggcatcgg agctgggacg gtgcgcgcct tcgtgaacag 200  
 cggggcccga gtggttatct gcgacaagga tgagtctggg ggccggggccc 250  
 tggagcagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300  
 gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttgccg 350  
 cctggattgt gttgtcaaca acgctggcca ccacccaccc ccacagaggc 400

total=1304700

ctgaggagac ctctgccag ggattccgcc agctgctgga gctgaaccta 450  
ctggggacgt acaccttgac caagctcgcc ctccctacc tgcggaagag 500  
tcaaggaat gtcataca tctccagcct ggtgggggca atcggccagg 550  
cccaggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600  
aaagctttgg ccctggatga aagtccatat ggtgtccgag tcaactgtat 650  
ctccccagga aacatctgga ccccgtgtg ggaggagctg gcagccttaa 700  
tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750  
ggccgcatgg gccagccgc tgaggtcggg gctgcggcag tggtcctggc 800  
ctccgaagcc aacttctgca cgggcattga actgctcgtg acggggggtg 850  
cagagctggg gtacgggtgc aaggccagtc ggagcacccc cgtggacgcc 900  
cccgatatcc ctctctgatt tctctcattt ctacttggg ccccttcct 950  
aggactctcc caccctaaac tccaacctgt atcagatgca gcccctaac 1000  
ccttagactc taagcccagt tagcaagggtg ccgggtcacc ctgcaggttc 1050  
ccataaaaac gatttgcagc c 1071

<210> 468  
<211> 270  
<212> PRT  
<213> Homo sapiens

<400> 468  
Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr  
1 5 10 15  
Gly Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val  
20 25 30  
Asn Ser Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly  
35 40 45  
Gly Arg Ala Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu  
50 55 60  
Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu  
65 70 75  
Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala  
80 85 90  
Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln  
95 100 105  
Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr  
110 115 120

Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn  
 125 130 135  
 Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln  
 140 145 150  
 Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr  
 155 160 165  
 Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn  
 170 175 180  
 Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp Glu Glu Leu  
 185 190 195  
 Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu Gly Met  
 200 205 210  
 Leu Ala Gln Pro Leu Gly Arg Met Gly Gln Pro Ala Glu Val Gly  
 215 220 225  
 Ala Ala Ala Val Phe Leu Ala Ser Glu Ala Asn Phe Cys Thr Gly  
 230 235 240  
 Ile Glu Leu Leu Val Thr Gly Gly Ala Glu Leu Gly Tyr Gly Cys  
 245 250 255  
 Lys Ala Ser Arg Ser Thr Pro Val Asp Ala Pro Asp Ile Pro Ser  
 260 265 270

<210> 469  
 <211> 687  
 <212> DNA  
 <213> Homo sapiens

<400> 469  
 aggcgggcag cagctgcagg ctgacctgac agcttgccgg aatggactgg 50  
 cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100  
 ccagcccagg agccccaaaa gcaagaggaa ggggcaagg cggcctgggc 150  
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200  
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250  
 ggcccagctg aggaacagct cagagctggc ccagagaaag tgtgaggtca 300  
 acttgacgct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350  
 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400  
 gtgcctgtgt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450  
 gcatggtgag cgtgccgtg ttcagccagg ttcctgtgcg ccgccgcctc 500  
 tgcccggcac cgccccgcac agggccttgc cgccagcgcg cagtcatgga 550



gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600  
 gccaggccag cagcccagaga ccatactcct tgcacctttg tgccaagaaa 650  
 ggccatgaa aagtaaaccac tgacttttga aagcaag 687

<210> 470  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

<400> 470  
 Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile  
 1 5 10 15  
 Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys  
 20 25 30  
 Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val  
 35 40 45  
 Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu  
 50 55 60  
 Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn  
 65 70 75  
 Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu  
 80 85 90  
 Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile  
 95 100 105  
 Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg  
 110 115 120  
 Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp  
 125 130 135  
 Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg  
 140 145 150  
 Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln  
 155 160 165  
 Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe  
 170 175 180

<210> 471  
 <211> 2368  
 <212> DNA  
 <213> Homo sapiens

<400> 471  
 gcgcccag gcgtaggcgg ggtggccctt gcgtctcccg cttccttgaa 50  
 aaacccggcg ggcgagcgag gctgcgggcc ggccgctgcc cttccccaca 100



cctgagcatc cccaaagtgt aacgtagaag ccttgcatcc ttttcttggtg 1600  
taaagtattt atttttgtca aattgcagga aacatcaggc accacagtgc 1650  
atgaaaaatc tttcacagct agaaattgaa agggccttgg gtatagagag 1700  
cagctcagaa gtcatcccag ccctctgaat ctctgtgtct atgttttatt 1750  
tcttaccttt aatttttcca gcatttccac catgggcatt caggctctcc 1800  
acactcttca ctattatctc ttggtcagag gactccaata acagccaggt 1850  
ttacatgaac tgtgtttggt cattctgacc taaggggttt agataatcag 1900  
taaccataac ccctgaagct gtgactgcc aacatctcaa atgaaatggt 1950  
gtggccatca gagactcaaa aggaagtaag gattttacaa gacagattaa 2000  
aaaaaaattg ttttgtccaa aatatagttg ttgttgattt tttttaagt 2050  
tttctaagca atatttttca agccagaagt cctctaagtc ttgccagtac 2100  
aaggtagtct tgtgaagaaa agttgaatac tgttttgttt tcatctcaag 2150  
gggttccttg ggtcttgaac tactttaata ataactaaaa aaccacttct 2200  
gattttcctt cagtgatgtg cttttggtga aagaattaat gaactccagt 2250  
acctgaaagt gaaagatttg attttgtttc catcttctgt aatcttccaa 2300  
agaattatat ctttgtaaat ctctcaatac tcaatctact gtaagtacc 2350  
aggaggcta atttcttt 2368

<210> 472  
<211> 349  
<212> PRT  
<213> Homo sapiens

<400> 472  
Met Ala Gly Gly Arg Cys Gly Pro Gln Leu Thr Ala Leu Leu Ala  
1 5 10 15  
Ala Trp Ile Ala Ala Val Ala Ala Thr Ala Gly Pro Glu Glu Ala  
20 25 30  
Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser  
35 40 45  
Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr  
50 55 60  
Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu  
65 70 75  
Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys  
80 85 90

Val Asp Val Ile Gln Glu Pro Gly Leu Ser Gly Arg Phe Phe Val  
 95 100 105  
 Thr Thr Leu Pro Ala Phe Phe His Ala Lys Asp Gly Ile Phe Arg  
 110 115 120  
 Arg Tyr Arg Gly Pro Gly Ile Phe Glu Asp Leu Gln Asn Tyr Ile  
 125 130 135  
 Leu Glu Lys Lys Trp Gln Ser Val Glu Pro Leu Thr Gly Trp Lys  
 140 145 150  
 Ser Pro Ala Ser Leu Thr Met Ser Gly Met Ala Gly Leu Phe Ser  
 155 160 165  
 Ile Ser Gly Lys Ile Trp His Leu His Asn Tyr Phe Thr Val Thr  
 170 175 180  
 Leu Gly Ile Pro Ala Trp Cys Ser Tyr Val Phe Phe Val Ile Ala  
 185 190 195  
 Thr Leu Val Phe Gly Leu Phe Met Gly Leu Val Leu Val Val Ile  
 200 205 210  
 Ser Glu Cys Phe Tyr Val Pro Leu Pro Arg His Leu Ser Glu Arg  
 215 220 225  
 Ser Glu Gln Asn Arg Arg Ser Glu Glu Ala His Arg Ala Glu Gln  
 230 235 240  
 Leu Gln Asp Ala Glu Glu Glu Lys Asp Asp Ser Asn Glu Glu Glu  
 245 250 255  
 Asn Lys Asp Ser Leu Val Asp Asp Glu Glu Glu Lys Glu Asp Leu  
 260 265 270  
 Gly Asp Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Asp Asn Leu  
 275 280 285  
 Ala Ala Gly Val Asp Glu Glu Arg Ser Glu Ala Asn Asp Gln Gly  
 290 295 300  
 Pro Pro Gly Glu Asp Gly Val Thr Arg Glu Glu Val Glu Pro Glu  
 305 310 315  
 Glu Ala Glu Glu Gly Ile Ser Glu Gln Pro Cys Pro Ala Asp Thr  
 320 325 330  
 Glu Val Val Glu Asp Ser Leu Arg Gln Arg Lys Ser Gln His Ala  
 335 340 345  
 Asp Lys Gly Leu

<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 473  
gtccagccca tgaccgcctc caac 24

<210> 474  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 474  
ctctcctcat ccacaccagc agcc 24

<210> 475  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 475  
gtggatgctg aaattttacg ccccatgggtg tccatcctgc cagc 44

<210> 476  
<211> 2478  
<212> DNA  
<213> Homo sapiens

<400> 476  
atctggttga actacttaag cttattttgt taaactccgg taagtacctta 50  
gcccacatga ttgactcag agattctctt ttgtccacag acagtcattct 100  
caggggcaga aagaaaagag ctcccaaag ctatatctat tcaggggctc 150  
tcaagaacaa tggaaatca tctgattta gaaaatttgg atgaagatgg 200  
atatactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250  
tttcagagaa aggatcgtgt gctgcatctc ctccttggcg cctcattgct 300  
gtaatttttg gaatcctatg cttggttaata ctggtgatag ctgtggctcct 350  
gggtaccatg ggggttcttt ccagcccttg tcctcctaata tggattatat 400  
atgagaagag ctgttatcta ttcagcatgt cactaaattc ctgggatgga 450  
agtaaaagac aatgctggca actgggctct aatctcctaa agatagacag 500  
ctcaaataga ttgggattta tagtaaaaca agtgtcttcc caacctgata 550  
attcattttg gataggcctt tctcggtccc agactgaggt accatggctc 600

tgggaggatg gatcaacatt ctcttctaac ttatttcaga tcagaaccac 650  
 agctacccaa gaaaacccat ctccaaattg tgtatggatt cacgtgtcag 700  
 tcatttatga ccaactgtgt agtgtgccct catatagtat ttgtgagaag 750  
 aagttttcaa tgtaagagga aggggtggaga aggagagaga aatatgtgag 800  
 gtagtaagga ggacagaaaa cagaacagaa aagagtaaca gctgagggtca 850  
 agataaatgc agaaaatggt tagagagctt ggccaactgt aatcttaacc 900  
 aagaaattga agggagaggc tgtgatttct gtatttgtcg acctacaggt 950  
 aggctagtat ttttttcta gttagtagat ccctagacat ggaatcaggg 1000  
 cagccaagct tgagttttta ttttttattt atttattttt ttgagatagg 1050  
 gtctcacttt gttaccaggc ctggagtgcg gtggcacaat ctgcactcac 1100  
 tgcagctatc tctgcctca gccctcaag tagctgggac tacagggtgca 1150  
 tgccaccatg ccaggctaatt ttttggtgtt tttttagag actgggtttt 1200  
 gccatgttga ccaagctggt ctctaactcc tgggcttaag tgatctgccc 1250  
 gccttggcct cccaaagtgc tgggattaca gatgtgagcc accacacctg 1300  
 gcccgaagct tgaattttca ttctgccatt gacttggcat ttaccttggg 1350  
 taagccataa gcgaatctta atttctggct ctatcagagt tgtttcatgc 1400  
 tcaacaatgc cattgaagtgc caggtgtgtg tgccacgatt tgaccctcaa 1450  
 cttctagcag tatatcagtt atgaactgag ggtgaaatat atttctgaat 1500  
 agctaaatga agaaatggga aaaaatcttc accacagtca gagcaatttt 1550  
 attattttca tcagtatgat cataattatg attatcatct tagtaaaaag 1600  
 caggaactcc tactttttct ttatcaatta aatagctcag agagtacatc 1650  
 tgccatatct ctaatagaat cttttttttt tttttttttt ttgagacag 1700  
 agtttcgctc ttgttgccca ggctggagtgc caacggcagc atctcggctc 1750  
 accgcaacct ccgccccctg ggttcaagca attctcctgc ctcagcctcc 1800  
 caagtagctg ggattacagt caggcaccac cacaccggc taattttgta 1850  
 tttttttagt agagacaggg tttctccatg tcggtcaggg tagtcccgaa 1900  
 ctctgacct caagtgatct gcctgcctcg gcctcccaag tgctgggatt 1950  
 acaggcgtga gccactgcac ccagcctaga atcttgtata atatgtaatt 2000  
 gtagggaaac tgctctcata ggaaagtttt ctgcttttta aatacaaaaa 2050

tacataaaaa tacataaaat ctgatgatga atataaaaaa gtaaccaacc 2100  
 tcattggaac aagtattaac attttgaat atgttttatt agttttgtga 2150  
 tgtactgttt tacaattttt accatttttt tcagtaatta ctgtaaaatg 2200  
 gtattattgg aatgaaacta tatttcctca tgtgctgatt tgtcttattt 2250  
 ttttcatact ttcccaactgg tgcatttttt atttccaatg gatattttctg 2300  
 tattactagg gaggcattta cagtcctcta atgttgatta atatgtgaaa 2350  
 agaaattgta ccaattttac taaattatgc agttttaaag ggatgatttt 2400  
 atgttatgtg gatttcattt caataaaaaa aaactcttat caaaaaaaaaa 2450  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2478

<210> 477  
 <211> 201  
 <212> PRT  
 <213> Homo sapiens

<400> 477  
 Met Glu Tyr His Pro Asp Leu Glu Asn Leu Asp Glu Asp Gly Tyr  
 1 5 10 15  
 Thr Gln Leu His Phe Asp Ser Gln Ser Asn Thr Arg Ile Ala Val  
 20 25 30  
 Val Ser Glu Lys Gly Ser Cys Ala Ala Ser Pro Pro Trp Arg Leu  
 35 40 45  
 Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile  
 50 55 60  
 Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro  
 65 70 75  
 Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met  
 80 85 90  
 Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu  
 95 100 105  
 Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe  
 110 115 120  
 Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile  
 125 130 135  
 Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp  
 140 145 150  
 Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala  
 155 160 165  
 Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser

170

175

180

Val Ile Tyr Asp Gln Leu Cys Ser Val Pro Ser Tyr Ser Ile Cys  
185 190 195

Glu Lys Lys Phe Ser Met  
200

&lt;210&gt; 478

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 478

gtccacagac agtcatctca ggagcag 27

&lt;210&gt; 479

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 479

acaagtgtct tccaacctg 20

&lt;210&gt; 480

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 480

atcctcccag agccatggta cctc 24

&lt;210&gt; 481

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 481

ccaaggatag ctgttggttc agagaaagga tcgtgtgctg catctcctcc 50

t 51

&lt;210&gt; 482

&lt;211&gt; 3819

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

340

T0120T 1802T00T





<400> 482

ggaaggggag gagcaggcca cacaggcaca ggccggtgag ggacctgccc 50  
agacctggag ggtctcgctc tgtcacacag gctggagtgc agtgggtgta 100  
tcttggtca tcgtaacctc cacctcccgg gttcaagtga ttctcatgcc 150  
tcagcctccc gagtagctgg gattacaggt ggtgacttcc aagagtgact 200  
ccgtcggagg aaaatgactc ccagtcgct gctgcagacg acactgttcc 250  
tgctgagtct gctcttctg gtccaaggtg cccacggcag gggccacagg 300  
gaagactttc gcttctgcag ccagcggaac cagacacaca ggagcagcct 350  
ccactacaaa cccacaccag acctgcgat ctccatcgag aactccgaag 400  
aggccctcac agtccatgcc cctttccctg cagccccacc tgcttccga 450  
tccttccctg accccagggg cctctaccac ttctgcctct actggaaccg 500  
acatgctggg agattacatc ttctctatgg caagcgtgac ttcttgctga 550  
gtgacaaagc ctctagctc ctctgcttcc agcaccagga ggagagcctg 600  
gtcaggggcc ccccgctgtt agccacttct gtcacctctt ggtggagccc 650  
tcagaacatc agcctgcca gtgcccag cttcaccttc tccttccaca 700  
gtcctcccca cagggcgct cacaatgcct cgggtggacat gtgcgagctc 750  
aaaagggacc tcagctgct cagccagttc ctgaagcatc cccagaaggc 800  
ctcaaggagg ccctcggtg ccccgccag ccagcagttg cagagcctgg 850  
agtcgaaact gacctctgtg agattcatgg gggacatggt gtccttcgag 900  
gaggaccgga tcaacgccac ggtgtggaag ctccagccca cagccggcct 950  
ccaggacctg cacatccact cccggcagga ggaggagcag agcgagatca 1000  
tgaggtactc ggtgctgctg cctcgaacac tcttccagag gacgaaaggc 1050  
cggagcgggg aggtgagaa gagactcctc ctggtggact tcagcagcca 1100  
agccctgttc caggacaaga attccagcca agtcctgggt gagaaggtct 1150  
tggggattgt ggtacagaac accaaagtag ccaacctcac ggagcccggtg 1200  
gtgctcactt tccagacca gctacagccg aagaatgtga ctctgcaatg 1250  
tgtgttctgg gttgaagacc ccacattgag cagcccgggg cattggagca 1300  
gtgctgggtg tgagaccgtc aggagagaaa cccaaacatc ctgcttctgc 1350  
aaccacttga cctactttgc agtgctgatg gtctcctcgg tggaggtgga 1400  
cgccgtgcac aagcactacc tgagcctcct ctctacgtg ggctgtgtcg 1450

TCAGCTGCTC

tctctgcctt ggccctgcctt gtcaccattg ccgcctacct ctgctccagg 1500  
 gtgcccctgc cgtgcaggag gaaacctcgg gactacacca tcaaggtgca 1550  
 catgaacctg ctgctggccg tcttctctgt ggacacgagc ttctgtctca 1600  
 gcgagccggg ggcctgaca ggctctgagg ctggctgccg agccagtgcc 1650  
 atcttctctg acttctccct gctcacctgc ctttcttgga tgggcctcga 1700  
 ggggtacaac ctctaccgac tcgtggtgga ggtctttggc acctatgtcc 1750  
 ctggctacct actcaagctg agcgccatgg gctggggctt ccccatcttt 1800  
 ctggtgacgc tgggtggcct ggtggatgtg gacaactatg gcccacatcat 1850  
 cttggtctgt cataggactc cagagggcgt catctaccct tccatgtgct 1900  
 ggatccggga ctccctggtc agctacatca ccaacctggg cctcttcagc 1950  
 ctgggtgttc tgttcaacat ggccatgcta gccaccatgg tgggtcagat 2000  
 cctgcggctg cgccccaca cccaaaagtg gtcacatgtg ctgacactgc 2050  
 tgggcctcag cctggctcctt ggccctgcctt gggccttgat cttcttctcc 2100  
 tttgtctctg gcaccttcca gcttgctcgtc ctctaccttt tcagcatcat 2150  
 cacctccttc caaggcttcc tcattctcat ctggtactgg tccatgcggc 2200  
 tgcaggcccg ggggtggccc tcccctctga agagcaactc agacagcgcc 2250  
 aggctcccca tcagctcggg cagcacctcg tccagccgca tctaggcctc 2300  
 cagcccacct gccatgtga tgaagcagag atgcggcctc gtcgcacact 2350  
 gctgtggcc cccgagccag gccagcccc aggccagtca gccgcagact 2400  
 ttggaagcc caacgacct ggagagatgg gccgttgcca tgggtggacgg 2450  
 actcccgggc tgggcttttg aattggcctt ggggactact cggctctcac 2500  
 tcagctccca cgggactcag aagtgcgcg ccatgctgcc tagggtactg 2550  
 tccccacatc tgtcccaacc cagctggagg cctggtctct ccttacaacc 2600  
 cctgggcca gccctcattg ctgggggcca ggccttgat cttgagggtc 2650  
 tggcacatcc ttaatcctgt gccctgcctt gggacagaaa tgtggctcca 2700  
 gttgctctgt ctctctggt caccctgagg gcaactctga tcctctgtca 2750  
 ttttaacctc aggtggcacc cagggcgaat ggggccagag gcagaccttc 2800  
 agggccagag ccctggcgga ggagaggccc tttgccagga gcacagcagc 2850  
 agctcgcta cctctgagcc caggccccct ccctccctca gccccccagt 2900



Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe	
				80					85					90	
Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	
				95					100					105	
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	
				110					115					120	
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	
				125					130					135	
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	
				140					145					150	
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	
				155					160					165	
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	
				170					175					180	
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	
				185					190					195	
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	
				200					205					210	
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	
				215					220					225	
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	
				230					235					240	
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	
				245					250					255	
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	
				260					265					270	
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	
				275					280					285	
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	
				290					295					300	
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	
				305					310					315	
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	
				320					325					330	
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	
				335					340					345	
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	
				350					355					360	
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	

TOPEL 15021001

365	370	375
Ser Cys Phe Cys Asn His Leu Thr Tyr	Phe Ala Val Leu Met Val	
380	385	390
Ser Ser Val Glu Val Asp Ala Val His	Lys His Tyr Leu Ser Leu	
395	400	405
Leu Ser Tyr Val Gly Cys Val Val Ser	Ala Leu Ala Cys Leu Val	
410	415	420
Thr Ile Ala Ala Tyr Leu Cys Ser Arg	Val Pro Leu Pro Cys Arg	
425	430	435
Arg Lys Pro Arg Asp Tyr Thr Ile Lys	Val His Met Asn Leu Leu	
440	445	450
Leu Ala Val Phe Leu Leu Asp Thr Ser	Phe Leu Leu Ser Glu Pro	
455	460	465
Val Ala Leu Thr Gly Ser Glu Ala Gly	Cys Arg Ala Ser Ala Ile	
470	475	480
Phe Leu His Phe Ser Leu Leu Thr Cys	Leu Ser Trp Met Gly Leu	
485	490	495
Glu Gly Tyr Asn Leu Tyr Arg Leu Val	Val Glu Val Phe Gly Thr	
500	505	510
Tyr Val Pro Gly Tyr Leu Leu Lys Leu	Ser Ala Met Gly Trp Gly	
515	520	525
Phe Pro Ile Phe Leu Val Thr Leu Val	Ala Leu Val Asp Val Asp	
530	535	540
Asn Tyr Gly Pro Ile Ile Leu Ala Val	His Arg Thr Pro Glu Gly	
545	550	555
Val Ile Tyr Pro Ser Met Cys Trp Ile	Arg Asp Ser Leu Val Ser	
560	565	570
Tyr Ile Thr Asn Leu Gly Leu Phe Ser	Leu Val Phe Leu Phe Asn	
575	580	585
Met Ala Met Leu Ala Thr Met Val Val	Gln Ile Leu Arg Leu Arg	
590	595	600
Pro His Thr Gln Lys Trp Ser His Val	Leu Thr Leu Leu Gly Leu	
605	610	615
Ser Leu Val Leu Gly Leu Pro Trp Ala	Leu Ile Phe Phe Ser Phe	
620	625	630
Ala Ser Gly Thr Phe Gln Leu Val Val	Leu Tyr Leu Phe Ser Ile	
635	640	645
Ile Thr Ser Phe Gln Gly Phe Leu Ile	Phe Ile Trp Tyr Trp Ser	
650	655	660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn  
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser  
680 685 690

Ser Arg Ile

<210> 484  
<211> 516  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 68, 70, 84, 147  
<223> unknown base

<400> 484  
tgcttgccct gccttgtaa caatgccgt tactctgctt ccaggttggc 50  
ctgccttgca gaggaanct tcgggactac accntcaagt gcacatgaac 100  
ctgctgctgg ccgtcttct gctggacacg agcttctgc tcagcgnagc 150  
cgggtggcct gacaggtct gaaggtggc tgccgagcca gtgccatctt 200  
cctgcacttc tctgctcac ctgcctttcc tggatgggccc tcgaggggta 250  
caacctctac cgactcgtgg tggaggtctt tggcacctat gtccctggct 300  
acctactcaa gctgagcgcc atgggctggg gcttcccat ctttctggtg 350  
acgctggtgg ccctggtgga tgtggacaac tatggcccca tcatcttggc 400  
tgtgcatagg actccagagg gcgtcatcta cccttccatg tgctggatcc 450  
gggactccct ggtcagctac atcaccaacc tgggcctctt cagcctggtg 500  
tttctgttca acatgg 516

<210> 485  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 485  
ggcattggag cagtgtggtg tg 22

<210> 486  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 486  
tggaggccta gatgcggctg gacg 24

<210> 487  
<211> 2849  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2715  
<223> unknown base

<400> 487  
cggacgcgtg ggcggacgcg tgggcgacg cgtggcgga cgcgtgggct 50  
ggttcaggctc caggttttgc ttgatcctt ttcaaaaact ggagacacag 100  
aagagggctc taggaaaaag ttttgatgg gattatgtgg aaactaccct 150  
gcgattctct gctgccagag caggctcggc gcttccaccc cagtgcagcc 200  
ttcccctggc ggtggtgaaa gagactcggg agtcgctgct tccaaagtgc 250  
ccgccgtgag tgagctctca cccagtcag ccaaagtgc ctcttcgggc 300  
ttctcctgct gacatctgcc ctggccggcc agagacaggg gactcaggcg 350  
gaatccaacc tgagtagtaa attccagttt tccagcaaca aggaacagaa 400  
cggagtacaa gatcctcagc atgagagaat tattactgtg tctactaatg 450  
gaagtattca cagcccaagg tttcctcata cttatccaag aaatacggtc 500  
ttggtatgga gattagtagc agtagaggaa aatgtatgga tacaacttac 550  
gtttgatgaa agatttgggc ttgaagaccc agaagatgac atatgcaagt 600  
atgattttgt agaagttgag gaaccagtg atggaactat attagggcgc 650  
tggtgtggtt ctggtactgt accaggaaaa cagatttcta aaggaaatca 700  
aattaggata agatttgtat ctgatgaata ttttccttct gaaccagggt 750  
tctgcatcca ctacaacatt gtcatgccac aattcacaga agctgtgagt 800  
ccttcagtgc taccoccttc agctttgcca ctggacctgc ttaataatgc 850  
tataactgcc ttagtacct tggaagacct tattcgatat cttgaaccag 900  
agagatggca gttgactta gaagatctat ataggccaac ttggcaactt 950  
cttggaagg cttttgtttt tggaagaaaa tccagagtgg tggatctgaa 1000  
ccttctaaca gaggaggtaa gattatacag ctgcacacct cgtaacttct 1050

cagtgtccat aaggaagaa ctaaagagaa ccgataccat tttctggcca 1100  
 ggttgtctcc tggtaaacg ctgtgtggg aactgtgcct gttgtctcca 1150  
 caattgcaat gaatgtcaat gtgtcccaag caaagttact aaaaaatacc 1200  
 acgaggtcct tcagttgaga ccaaagaccg gtgtcagggg attgcacaaa 1250  
 tcactcaccg acgtggccct ggagcaccat gaggagtgtg actgtgtgtg 1300  
 cagagggagc acaggaggat agccgcacat ccaccagcag ctcttgccca 1350  
 gagctgtgca gtgcagtggc tgattctatt agagaacgta tgcgttatct 1400  
 ccatccttaa tctcagttgt ttgcttcaag gacctttcat cttcaggatt 1450  
 tacagtgcac tctgaaagag gagacatcaa acagaattag gagttgtgca 1500  
 acagctcttt tgagaggagg cctaaaggac aggagaaaag gtcttcaatc 1550  
 gtggaagaa aattaaatgt tgtattaaat agatcaccag ctagtttcag 1600  
 agttaccatg tacgtattcc actagctggg ttctgtatct cagttctttc 1650  
 gatacggcct agggtaatgt cagtacagga aaaaaactgt gcaagtgagc 1700  
 acctgattcc gttgccttgc ttaactctaa agctccatgt cctgggccta 1750  
 aaatcgtata aaatctggat tttttttttt ttttttgctc atattcacat 1800  
 atgtaaacca gaacattcta tgtactaaa acctgggttt taaaaaggaa 1850  
 ctatgttgct atgaattaaa cttgtgtcat gctgatagga cagactggat 1900  
 ttttcatatt tcttattaaa atttctgcca tttagaagaa gagaactaca 1950  
 ttcattggtt ggaagagata aacctgaaa gaagagtggc cttatcttca 2000  
 ctttatcgat aagtcagttt atttgtttca ttgtgtacat ttttatattc 2050  
 tccttttgac attataactg ttggcttttc taatcttgtt aaatatatct 2100  
 atttttacca aaggtattta atattctttt ttatgacaac ttagatcaac 2150  
 tatttttagc ttggtaaatt tttctaaaca caattgttat agccagagga 2200  
 acaaagatga tataaaatat tgttgctctg acaaaaatac atgtatttca 2250  
 ttctcgtatg gtgctagagt tagattaatc tgcattttta aaaactgaat 2300  
 tggaatagaa ttggtaagtt gcaaagactt ttgaaaata attaaattat 2350  
 catatcttcc attcctgtta ttggagatga aaataaaaag caacttatga 2400  
 aagtagacat tcagatccag ccattactaa cctattcctt ttttggggaa 2450  
 atctgagcct agctcagaaa aacataaagc accttgaaaa agacttgcca 2500



gcttctgat aaagcgtgct gtgctgtgca gtaggaacac atcctattta 2550  
 ttgtgatgtt gtggttttat tatcttaaac tctgttccat acacttgat 2600  
 aaatacatgg atatttttat gtacagaagt atgtctctta accagttcac 2650  
 ttattgtact ctggcaattt aaaagaaaat cagtaaaata ttttgcttgt 2700  
 aaaatgctta atatngtgcc taggttatgt ggtgactatt tgaatcaaaa 2750  
 atgtattgaa tcatcaaaata aaagaatgtg gctattttgg ggagaaaatt 2800  
 aaaaaaaaaa aaaaaaaaaa aggtttaggg ataacagggt aatgcggcc 2849

<210> 488  
 <211> 345  
 <212> PRT  
 <213> Homo sapiens

<400> 488

Met	Ser	Leu	Phe	Gly	Leu	Leu	Leu	Leu	Thr	Ser	Ala	Leu	Ala	Gly
1				5					10					15
Gln	Arg	Gln	Gly	Thr	Gln	Ala	Glu	Ser	Asn	Leu	Ser	Ser	Lys	Phe
				20					25					30
Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln
				35					40					45
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser
				50					55					60
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp
				65					70					75
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe
				80					85					90
Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys
				95					100					105
Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu
				110					115					120
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser
				125					130					135
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe
				140					145					150
Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro
				155					160					165
Gln	Phe	Thr	Glu	Ala	Val	Ser	Pro	Ser	Val	Leu	Pro	Pro	Ser	Ala
				170					175					180
Leu	Pro	Leu	Asp	Leu	Leu	Asn	Asn	Ala	Ile	Thr	Ala	Phe	Ser	Thr
				185					190					195

Leu	Glu	Asp	Leu	Ile	Arg	Tyr	Leu	Glu	Pro	Glu	Arg	Trp	Gln	Leu
				200					205					210
Asp	Leu	Glu	Asp	Leu	Tyr	Arg	Pro	Thr	Trp	Gln	Leu	Leu	Gly	Lys
				215					220					225
Ala	Phe	Val	Phe	Gly	Arg	Lys	Ser	Arg	Val	Val	Asp	Leu	Asn	Leu
				230					235					240
Leu	Thr	Glu	Glu	Val	Arg	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe
				245					250					255
Ser	Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe
				260					265					270
Trp	Pro	Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala
				275					280					285
Cys	Cys	Leu	His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Ser	Lys
				290					295					300
Val	Thr	Lys	Lys	Tyr	His	Glu	Val	Leu	Gln	Leu	Arg	Pro	Lys	Thr
				305					310					315
Gly	Val	Arg	Gly	Leu	His	Lys	Ser	Leu	Thr	Asp	Val	Ala	Leu	Glu
				320					325					330
His	His	Glu	Glu	Cys	Asp	Cys	Val	Cys	Arg	Gly	Ser	Thr	Gly	Gly
				335					340					345

$\langle 220 \rangle$

<223> Synthetic oligonucleotide probe

<400> 491  
caccacagcg tttaaccagg 20

<210> 492  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 492  
acaacaggca cagttcccac 20

<210> 493  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 493  
ggcggaatcc aacctgagta g 21

<210> 494  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 494  
gcggctatcc tctgtgctc 20

<210> 495  
<211> 3283  
<212> DNA  
<213> Homo sapiens

<400> 495  
cccatctcaa gctgatcttg gcacctctca tgctctgctc tttcaacca 50  
gacctctaca ttccattttg gaagaagact aaaaatggtg tttcaatgt 100  
ggacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150  
aaactccttg gggctagatg gtttcctaaa actctgccct gtgatgtcac 200  
tctggatgtt ccaaagaacc atgtgatcgt ggactgcaca gacaagcatt 250  
tgacagaaat tcttgagggt attcccacga acaccacgaa cctcaccctc 300  
accattaacc acataaccaga catctcccca gcgtcctttc acagactgga 350

ccatctggta gagatcgatt tcagatgcaa ctgtgtacct attccactgg 400  
 ggtcaaaaaa caacatgtgc atcaagaggc tgcagattaa acccagaagc 450  
 tttagtggac tcacttattt aaaatccctt tacctggatg gaaaccagct 500  
 actagagata ccgcagggcc tcccgcctag cttacagctt ctcagccttg 550  
 aggccaacaa catcttttcc atcagaaaag agaacttaac agaactggcc 600  
 aacatagaaa tactctacct gggccaaaac tgttattatc gaaatccttg 650  
 ttatgtttca tattcaatag agaaagatgc cttcctaaac ttgacaaagt 700  
 taaaagtgtc ctccctgaaa gataacaatg tcacagccgt ccctactgtt 750  
 ttgccatcta cttaacaga actatatctc tacaacaaca tgattgcaaa 800  
 aatccaagaa gatgatttta-ataacctcaa ccaattacaa attcttgacc 850  
 taagtggaaa ttgccctcgt tgttataatg ccccatcttc ttgtgcgccg 900  
 tgtaaaaata attctcccct acagatccct gtaaatgctt ttgatgcgct 950  
 gacagaatta aaagttttac gtctacacag taactctctt cagcatgtgc 1000  
 cccaagatg gttaagaac atcaacaac tccaggaact ggatctgtcc 1050  
 caaaacttct tggccaaaga aattggggat gctaaatttc tgcattttct 1100  
 cccagcctc atccaattgg atctgtcttt caattttgaa cttcaggtct 1150  
 atcgtgcac tatgaatcta tcacaagcat tttcttcaact gaaagcctg 1200  
 aaaattctgc ggatcagagg atatgtcttt aaagagtga aaagctttaa 1250  
 cctctgcga ttacataatc ttcaaaatct tgaagtctt gatcttgca 1300  
 ctaactttat aaaaattgct aacctcagca tgtttaaaca atttaaaaga 1350  
 ctgaaagtca tagatcttcc agtgaataaa atatcacctt caggagattc 1400  
 aagtgaagtt ggcttctgct caaatgccag aacttctgta gaaagttatg 1450  
 aaccccaggt cctggaacaa ttacattatt tcagatatga taagtatgca 1500  
 aggagttgca gattcaaaaa caaagaggct tctttcatgt ctgttaatga 1550  
 aagctgtac aagtatggc agaccttga tctaagtaaa aatagtatat 1600  
 tttttgtcaa gtctctgat tttcagcatc tttcttccct caaatgcctg 1650  
 aatctgtcag gaaatctcat tagccaaact cttaatggca gtgaattcca 1700  
 accttagca gagctgagat atttggaact ctccaacaac cggttgatt 1750  
 tactccattc aacagcattt gaagagcttc aaaaactgga agttctggat 1800

ataagcagta atagccatta ttttcaatca gaaggaatta ctcatatgct 1850  
 aaactttacc aagaacctaa aggttctgca gaaactgatg atgaacgaca 1900  
 atgacatctc ttcctccacc agcaggacca tggagagtga gtctcttaga 1950  
 actctggaat tcagaggaaa tcacttagat gttttatgga gagaaggtga 2000  
 taacagatac ttacaattat tcaagaatct gctaaaatta gaggaattag 2050  
 acatctctaa aaattcccta agtttcttgc cttctggagt ttttgatggg 2100  
 atgcctccaa atctaaagaa tctctctttg gccaaaaatg ggctcaaadc 2150  
 tttcagttgg aagaaactcc agtgtctaaa gaacctggaa actttggacc 2200  
 tcagccacaa ccaactgacc actgtccctg agagattatc caactgttcc 2250  
 agaagcctca agaactctgat tcttaagaat aatcaaatca ggagtctgac 2300  
 gaagtatttt ctacaagatg ccttccagtt gcgatctctg gatctcagct 2350  
 caaataaaat ccagatgac caaaagacca gcttcccaga aaatgtcctc 2400  
 aacaatctga agatgttgct tttgcatcat aatcggtttc tgtgcacctg 2450  
 tgatgctgtg tggtttgtct ggtggggtta ccatacggag gtgactattc 2500  
 cttacctggc cacagatgtg acttgtgtgg gccaggagc acacaagggc 2550  
 caaagtgtga tctccctgga tctgtacacc tgtgagttag atctgactaa 2600  
 cctgattctg ttctcacttt ccatactgt atctctcttt ctcatggtga 2650  
 tgatgacagc aagtcacctc tatttctggg atgtgtggta tatttaccat 2700  
 ttctgtaagg ccaagataaa ggggtatcag cgtctaatat caccagactg 2750  
 ttgctatgat gcttttattg tgtatgacac taaagaccca gctgtgaccg 2800  
 agtgggtttt ggctgagctg gtggccaaac tggaaagacc aagagagaaa 2850  
 cattttaatt tatgtctcga ggaaagggac tggttaccag ggcagccagt 2900  
 tctggaaaac ctttcccaga gcatacagct tagcaaaaag acagtgtttg 2950  
 tgatgacaga caagtatgca aagactgaaa attttaagat agcattttac 3000  
 ttgtccatc agaggctcat ggatgaaaaa gttgatgtga ttatcttgat 3050  
 atttcttgag aagccctttc agaagtccaa gttcctccag ctccggaaaa 3100  
 ggctctgtgg gagttctgtc cttgagtggc caacaaaccc gcaagctcac 3150  
 ccatacttct ggcagtgtct aaagaacgcc ctggccacag acaatcatgt 3200  
 ggcttatagt caggtgttca aggaaacggt ctagcccttc ttgcaaaac 3250

acaactgcct agtttaccaa ggagaggcct ggc 3283

<210> 496

<211> 1049

<212> PRT

<213> Homo sapiens

<400> 496

Met Val Phe Pro Met Trp Thr Leu Lys Arg Gln Ile Leu Ile Leu  
1 5 10 15

Phe Asn Ile Ile Leu Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe  
20 25 30

Pro Lys Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn  
35 40 45

His Val Ile Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro  
50 55 60

Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn  
65 70 75

His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His  
80 85 90

Leu Val Glu Ile Asp Phe Arg Cys Asn Cys Val Pro Ile Pro Leu  
95 100 105

Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro  
110 115 120

Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu Tyr Leu Asp  
125 130 135

Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu  
140 145 150

Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys  
155 160 165

Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly  
170 175 180

Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile  
185 190 195

Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser  
200 205 210

Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser  
215 220 225

Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile  
230 235 240

Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp  
245 250 255

FORNEX-1300000

Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys  
 260 265 270  
 Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala  
 275 280 285  
 Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn  
 290 295 300  
 Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys  
 305 310 315  
 Leu Gln Glu Leu Asp Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile  
 320 325 330  
 Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu  
 335 340 345  
 Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr Arg Ala Ser Met  
 350 355 360  
 Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu  
 365 370 375  
 Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu  
 380 385 390  
 Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly  
 395 400 405  
 Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe  
 410 415 420  
 Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro  
 425 430 435  
 Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr  
 440 445 450  
 Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr  
 455 460 465  
 Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys  
 470 475 480  
 Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly  
 485 490 495  
 Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser  
 500 505 510  
 Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser  
 515 520 525  
 Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro  
 530 535 540  
 Leu Ala Glu Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp

545	550	555
Leu Leu His Ser Thr Ala Phe Glu Glu	Leu His Lys Leu Glu Val	
560	565	570
Leu Asp Ile Ser Ser Asn Ser His Tyr Phe Gln Ser Glu Gly Ile		
575	580	585
Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys Val Leu Gln Lys		
590	595	600
Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr Ser Arg Thr		
605	610	615
Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly Asn His		
620	625	630
Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln Leu		
635	640	645
Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn		
650	655	660
Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro		
665	670	675
Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe		
680	685	690
Ser Trp Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp		
695	700	705
Leu Ser His Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn		
710	715	720
Cys Ser Arg Ser Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile		
725	730	735
Arg Ser Leu Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg		
740	745	750
Tyr Leu Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr		
755	760	765
Ser Phe Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu		
770	775	780
His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val		
785	790	795
Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr		
800	805	810
Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val		
815	820	825
Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp Leu Thr Asn Leu		
830	835	840



Ile	Leu	Phe	Ser	Leu	Ser	Ile	Ser	Val	Ser	Leu	Phe	Leu	Met	Val	845	850	855
Met	Met	Thr	Ala	Ser	His	Leu	Tyr	Phe	Trp	Asp	Val	Trp	Tyr	Ile	860	865	870
Tyr	His	Phe	Cys	Lys	Ala	Lys	Ile	Lys	Gly	Tyr	Gln	Arg	Leu	Ile	875	880	885
Ser	Pro	Asp	Cys	Cys	Tyr	Asp	Ala	Phe	Ile	Val	Tyr	Asp	Thr	Lys	890	895	900
Asp	Pro	Ala	Val	Thr	Glu	Trp	Val	Leu	Ala	Glu	Leu	Val	Ala	Lys	905	910	915
Leu	Glu	Asp	Pro	Arg	Glu	Lys	His	Phe	Asn	Leu	Cys	Leu	Glu	Glu	920	925	930
Arg	Asp	Trp	Leu	Pro	Gly	Gln	Pro	Val	Leu	Glu	Asn	Leu	Ser	Gln	935	940	945
Ser	Ile	Gln	Leu	Ser	Lys	Lys	Thr	Val	Phe	Val	Met	Thr	Asp	Lys	950	955	960
Tyr	Ala	Lys	Thr	Glu	Asn	Phe	Lys	Ile	Ala	Phe	Tyr	Leu	Ser	His	965	970	975
Gln	Arg	Leu	Met	Asp	Glu	Lys	Val	Asp	Val	Ile	Ile	Leu	Ile	Phe	980	985	990
Leu	Glu	Lys	Pro	Phe	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	995	1000	1005
Arg	Leu	Cys	Gly	Ser	Ser	Val	Leu	Glu	Trp	Pro	Thr	Asn	Pro	Gln	1010	1015	1020
Ala	His	Pro	Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Ala	Thr	1025	1030	1035
Asp	Asn	His	Val	Ala	Tyr	Ser	Gln	Val	Phe	Lys	Glu	Thr	Val		1040	1045	

<210> 497

<211> 4199

<212> DNA

<213> Homo sapiens

<400> 497

gggtaccatt ctgcgctgct gcaagttacg gaatgaaaa ttagaacaac 50

agaaacatgg aaaacatggt ccttcagtcg tcaatgctga cctgcatttt 100

cctgctaata tctggttcct gtgagttatg cgccgaagaa aatttttcta 150

gaagctatcc ttgtgatgag aaaaagcaaa atgactcagt tattgcagag 200

tgacgaatc gtcgactaca ggaagttccc caaacggtgg gcaaatatgt 250

gacagaacta gacctgtctg ataatttcat cacacacata acgaatgaat 300  
catttcaagg gctgcaaaat ctactataaa taaatctaaa ccacaacccc 350  
aatgtacagc accagaacgg aaatcccggg atacaatcaa atggcttgaa 400  
tatcacagac ggggcattcc tcaacctaaa aaacctagg gagttactgc 450  
ttgaagacaa ccagttaccc caaataccct ctggtttgcc agagtctttg 500  
acagaactta gtctaattca aaacaatata tacaacataa ctaaagaggg 550  
catttcaaga cttataaact tgaaaaatct ctatttgcc tggaactgct 600  
atthtaacaa agtttgagag aaaactaaca tagaagatgg agtatttgaa 650  
acgtgacaa atttgaggt gctatcacta tctttcaatt ctctttcaca 700  
cgtgccacc aaactgccaa gctccctacg caaactttt ctgagcaaca 750  
cccagatcaa atacattagt gaagaagatt tcaagggatt gataaattta 800  
acattactag atttaagcgg gaactgtccg aggtgcttca atgccccatt 850  
tccatgcgtg ccttgatgag gtggtgcttc aattaatata gatcgttttg 900  
cttttcaaaa cttgaccaa cttcgatacc taaacctctc tagcacttcc 950  
ctcaggaaga ttaatgtgc ctggtttaaa aatatgcctc atctgaaggt 1000  
gctggatctt gaattcaact atttagtggg agaaatagtc tctggggcat 1050  
ttttaacgat gctgccccgc ttagaataac ttgactgtc ttttaactat 1100  
ataaagggga gttatccaca gcatattaat atttccagaa acttctctaa 1150  
acttttgtct ctacgggcat tgcatttaag aggttatgtg ttccaggaac 1200  
tcagagaaga tgatttccag cccctgatgc agcttccaaa cttatcgact 1250  
atcaacttgg gtattaattt tattaagcaa atcgatttca aacttttcca 1300  
aaatttctcc aatctgaaa ttatttactt gtcagaaaac agaatatcac 1350  
cgttggtaaa agatacccg cagagttatg caaatagttc ctcttttcaa 1400  
cgtcatatcc ggaaacgacg ctcaacagat ttgagtttg acccacattc 1450  
gaacttttat catttcaccc gtcctttaat aaagccacaa tgtgctgctt 1500  
atggaaaagc cttagattta agcctcaaca gtattttctt cattgggcca 1550  
aaccaatttg aaaatcttcc tgacattgcc tgtttaaatc tgtctgcaa 1600  
tagcaatgct caagtgttaa gtggaactga attttcagcc attcctcatg 1650  
tcaaatattt ggatttgaca aacaatagac tagactttga taatgctagt 1700



atatgtatgt cgattccatt aagcaatact aactgacgtt aagtcattgat 3200  
 ttgcgcgccat aataaagatg caaaggaatg acattttctgt attagttatc 3250  
 tattgctatg taacaaatta tcccaaaact tagtggttta aaacaacaca 3300  
 tttgctggcc cacagttttt gagggtcagg agtccaggcc cagcataact 3350  
 gggtcctctg ctcagggtgt ctcagaggct gcaatgtagg tggtcaccag 3400  
 agacataggc atcactgggg tcacactcat gtggttggtt tctggattca 3450  
 attcctcctg ggctattggc caaaggctat actcatgtaa gccatgcgag 3500  
 cctctccac aaggcagctt gcttcacag agctagcaaa aaagagaggt 3550  
 tgctagcaag atgaagtcac aatcttttgt aatcgaatca aaaaagtgat 3600  
 atctcatcac ttggccata ttctatttgt tagaagtaaa ccacaggtcc 3650  
 caccagctcc atgggagtga ccacctcagt ccagggaaaa cagctgaaga 3700  
 ccaagatggt gagctctgat tgcttcagtt ggtcatcaac tattttccct 3750  
 tgactgctgt cctgggatgg cctgctatct tgatgataga ttgtgaatat 3800  
 caggaggcag ggatcactgt ggaccatctt agcagttgac ctaacacatc 3850  
 ttcttttcaa tatctaagaa cttttgccac tgtgactaat ggtcctaata 3900  
 ttaagctggt gtttatattt atcatatata tatggctaca tggttatatt 3950  
 atgctgtggt tgcgttcggt tttatttaca gttgctttta caaatatttg 4000  
 ctgtaacatt tgacttctaa ggttttagatg ccatttaaga actgagatgg 4050  
 atagctttta aagcatcttt tacttcttac cattttttta aagtatgcag 4100  
 ctaaattcga agcttttggt ctatattggt aattgccatt gctgtaaatc 4150  
 ttaaatgaa tgaataaaaa tgtttcattt tacaaaaaaa aaaaaaaaa 4199

<210> 498  
 <211> 1041  
 <212> PRT  
 <213> Homo sapiens

<400> 498  
 Met Glu Asn Met Phe Leu Gln Ser Ser Met Leu Thr Cys Ile Phe  
 1 5 10 15  
 Leu Leu Ile Ser Gly Ser Cys Glu Leu Cys Ala Glu Glu Asn Phe  
 20 25 30  
 Ser Arg Ser Tyr Pro Cys Asp Glu Lys Lys Gln Asn Asp Ser Val  
 35 40 45  
 Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr

50	55	60
Val Gly Lys Tyr	Val Thr Glu Leu Asp	Leu Ser Asp Asn Phe Ile
65	70	75
Thr His Ile Thr	Asn Glu Ser Phe Gln Gly	Leu Gln Asn Leu Thr
80	85	90
Lys Ile Asn Leu	Asn His Asn Pro Asn Val	Gln His Gln Asn Gly
95	100	105
Asn Pro Gly Ile	Gln Ser Asn Gly Leu Asn	Ile Thr Asp Gly Ala
110	115	120
Phe Leu Asn Leu	Lys Asn Leu Arg Glu Leu	Leu Leu Glu Asp Asn
125	130	135
Gln Leu Pro Gln	Ile Pro Ser Gly Leu Pro	Glu Ser Leu Thr Glu
140	145	150
Leu Ser Leu Ile	Gln Asn Asn Ile Tyr Asn	Ile Thr Lys Glu Gly
155	160	165
Ile Ser Arg Leu	Ile Asn Leu Lys Asn Leu	Tyr Leu Ala Trp Asn
170	175	180
Cys Tyr Phe Asn	Lys Val Cys Glu Lys Thr	Asn Ile Glu Asp Gly
185	190	195
Val Phe Glu Thr	Leu Thr Asn Leu Glu Leu	Leu Ser Leu Ser Phe
200	205	210
Asn Ser Leu Ser	His Val Pro Pro Lys Leu	Pro Ser Ser Leu Arg
215	220	225
Lys Leu Phe Leu	Ser Asn Thr Gln Ile Lys	Tyr Ile Ser Glu Glu
230	235	240
Asp Phe Lys Gly	Leu Ile Asn Leu Thr Leu	Leu Asp Leu Ser Gly
245	250	255
Asn Cys Pro Arg	Cys Phe Asn Ala Pro Phe	Pro Cys Val Pro Cys
260	265	270
Asp Gly Gly Ala	Ser Ile Asn Ile Asp Arg	Phe Ala Phe Gln Asn
275	280	285
Leu Thr Gln Leu	Arg Tyr Leu Asn Leu Ser	Ser Thr Ser Leu Arg
290	295	300
Lys Ile Asn Ala	Ala Trp Phe Lys Asn Met	Pro His Leu Lys Val
305	310	315
Leu Asp Leu Glu	Phe Asn Tyr Leu Val Gly	Glu Ile Val Ser Gly
320	325	330
Ala Phe Leu Thr	Met Leu Pro Arg Leu Glu	Ile Leu Asp Leu Ser
335	340	345

Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile Asn Ile Ser  
 350 355 360  
 Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His Leu Arg  
 365 370 375  
 Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro Leu  
 380 385 390  
 Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe  
 395 400 405  
 Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu  
 410 415 420  
 Glu Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro Leu Val Lys  
 425 430 435  
 Asp Thr Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His  
 440 445 450  
 Ile Arg Lys Arg Arg Ser Thr Asp Phe Glu Phe Asp Pro His Ser  
 455 460 465  
 Asn Phe Tyr His Phe Thr Arg Pro Leu Ile Lys Pro Gln Cys Ala  
 470 475 480  
 Ala Tyr Gly Lys Ala Leu Asp Leu Ser Leu Asn Ser Ile Phe Phe  
 485 490 495  
 Ile Gly Pro Asn Gln Phe Glu Asn Leu Pro Asp Ile Ala Cys Leu  
 500 505 510  
 Asn Leu Ser Ala Asn Ser Asn Ala Gln Val Leu Ser Gly Thr Glu  
 515 520 525  
 Phe Ser Ala Ile Pro His Val Lys Tyr Leu Asp Leu Thr Asn Asn  
 530 535 540  
 Arg Leu Asp Phe Asp Asn Ala Ser Ala Leu Thr Glu Leu Ser Asp  
 545 550 555  
 Leu Glu Val Leu Asp Leu Ser Tyr Asn Ser His Tyr Phe Arg Ile  
 560 565 570  
 Ala Gly Val Thr His His Leu Glu Phe Ile Gln Asn Phe Thr Asn  
 575 580 585  
 Leu Lys Val Leu Asn Leu Ser His Asn Asn Ile Tyr Thr Leu Thr  
 590 595 600  
 Asp Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe  
 605 610 615  
 Ser Gly Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asp Asn Arg  
 620 625 630  
 Tyr Ile Ser Ile Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp

635	640	645
Leu Ser Leu Asn Arg Leu Lys His Ile	Pro Asn Glu Ala Phe Leu	
650	655	660
Asn Leu Pro Ala Ser Leu Thr Glu Leu	His Ile Asn Asp Asn Met	
665	670	675
Leu Lys Phe Phe Asn Trp Thr Leu Leu	Gln Gln Phe Pro Arg Leu	
680	685	690
Glu Leu Leu Asp Leu Arg Gly Asn Lys	Leu Leu Phe Leu Thr Asp	
695	700	705
Ser Leu Ser Asp Phe Thr Ser Ser Leu	Arg Thr Leu Leu Leu Ser	
710	715	720
His Asn Arg Ile Ser His Leu Pro Ser	Gly Phe Leu Ser Glu Val	
725	730	735
Ser Ser Leu Lys His Leu Asp Leu Ser	Ser Asn Leu Leu Lys Thr	
740	745	750
Ile Asn Lys Ser Ala Leu Glu Thr Lys	Thr Thr Thr Lys Leu Ser	
755	760	765
Met Leu Glu Leu His Gly Asn Pro Phe	Glu Cys Thr Cys Asp Ile	
770	775	780
Gly Asp Phe Arg Arg Trp Met Asp Glu	His Leu Asn Val Lys Ile	
785	790	795
Pro Arg Leu Val Asp Val Ile Cys Ala	Ser Pro Gly Asp Gln Arg	
800	805	810
Gly Lys Ser Ile Val Ser Leu Glu Leu	Thr Thr Cys Val Ser Asp	
815	820	825
Val Thr Ala Val Ile Leu Phe Phe Phe	Thr Phe Phe Ile Thr Thr	
830	835	840
Met Val Met Leu Ala Ala Leu Ala His	His Leu Phe Tyr Trp Asp	
845	850	855
Val Trp Phe Ile Tyr Asn Val Cys Leu	Ala Lys Val Lys Gly Tyr	
860	865	870
Arg Ser Leu Ser Thr Ser Gln Thr Phe	Tyr Asp Ala Tyr Ile Ser	
875	880	885
Tyr Asp Thr Lys Asp Ala Ser Val Thr	Asp Trp Val Ile Asn Glu	
890	895	900
Leu Arg Tyr His Leu Glu Glu Ser Arg	Asp Lys Asn Val Leu Leu	
905	910	915
Cys Leu Glu Glu Arg Asp Trp Asp Pro	Gly Leu Ala Ile Ile Asp	
920	925	930

Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val  
 935 940 945  
 Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe  
 950 955 960  
 Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile  
 965 970 975  
 Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu  
 980 985 990  
 Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro  
 995 1000 1005  
 Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn  
 1010 1015 1020  
 Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val  
 1025 1030 1035  
 Asp Ser Ile Lys Gln Tyr  
 1040

T  
O  
T  
A  
L  
L  
E  
N  
G  
T  
H  
:  
1  
0  
4  
0

<210> 499  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 499  
 taaagaccca gctgtgaccg 20

<210> 500  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 500  
 atccatgagc ctctgatggg 20

<210> 501  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 501  
 atttatgtct cgaggaaagg gactgggttac cagggcagcc agttc 45

<210> 502



<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 502  
gccgagacaa aaacgttctc c 21

<210> 503  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 503  
catccatggt ctcattccatt agcc 24

<210> 504  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 504  
tcgacaacct catgcagagc atcaacacaa gcaagaaaac agtatt 46

<210> 505  
<211> 1738  
<212> DNA  
<213> Homo sapiens

<400> 505  
ccagggtccaa ctgcacctcg gttctatcga ttgaattccc cggggatcct 50  
ctagagatcc ctcgacctcg acccaacgct ccgccaagct ggccctgcac 100  
ggctgcaagg gaggctcctg tggacaggcc aggcagggtg gcctcaggag 150  
gtgcctccag gcgccagtg ggcctgaggc ccagcaagg gctagggtcc 200  
atctccagtc ccaggacaca gcagcggcca ccatggccac gcctgggctc 250  
cagcagcatc agcagcccc aggaccgggg aggcacaggt ggccccacc 300  
accggaggga gcagctcctg cccctgtccg ggggatgact gattctctc 350  
cgccaggcca ccagaggag aaggccacc cgctggagg cacaggccat 400  
gaggggctct caggaggtgc tgctgatgtg gcttctggtg ttggcagtgg 450  
gcggcacaga gcacgcctac cggcccgcc gtaggggtg tgctgtccg 500

gctcacgggg accctgtctc cgagtcgttc gtgcagcgtg tgtaccagcc 550  
cttcctcacc acctgcgacg ggcaccgggc ctgcagcacc taccgaacca 600  
tctataggac cgcctaccgc cgcagccctg ggctggcccc tgccaggcct 650  
cgctacgcgt gctgccccgg ctggaagagg accagcgggc ttcctggggc 700  
ctgtggagca gcaatatgcc agccgccatg ccggaacgga gggagctgtg 750  
tccagcctgg ccgctgccgc tgcctgcag gatggcgggg tgacacttgc 800  
cagtcagatg tggatgaatg cagtgcctagg aggggcggct gtccccagcg 850  
ctgcatcaac accgccggca gttactggtg ccagtgttgg gaggggcaca 900  
gcctgtctgc agacgtaca ctctgtgtgc ccaaggagg gccccccagg 950  
gtggcccca acccgacagg agtggacagt gcaatgaagg aagaagtga 1000  
gaggctgcag tccagggtgg acctgctgga ggagaagctg cagctggtgc 1050  
tgccccact gcacagcctg gcctcgcagg cactggagca tgggctccc 1100  
gaccccgga gcctcctggt gactccttc cagcagctcg gccgcatcga 1150  
ctccctgagc gagcagattt ccttcctgga ggagcagctg gggctcctgct 1200  
cctgcaagaa agactcgtga ctgccagcg cccaggtcg gactgagccc 1250  
ctcacgccgc cctgcagccc ccattgccct gcccaacatg ctgggggtcc 1300  
agaagccacc tcggggtgac tgagcggaag gccaggcagg gccttcctcc 1350  
tcttcctcct ccccttcctc gggaggctcc ccagaccctg gcatgggatg 1400  
ggctgggatc ttctctgtga atccaccct ggctaccccc accctggcta 1450  
ccccaacggc atccaaggc caggtgggcc ctgagctgag ggaaggtacg 1500  
agctccctgc tggagcctgg gacccatggc acaggccagg cagcccggag 1550  
gctgggtggg gcctcagtgg ggctgctgc ctgaccccca gcacaataaa 1600  
aatgaaacgt gaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1650  
aaagggcggc cgcgactcta gagtcgacct gcagaagctt ggccgccatg 1700  
gccaacttg ttattgcag cttataatgg ttacaaat 1738

<210> 506  
<211> 273  
<212> PRT  
<213> Homo sapiens

<400> 506  
Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu  
1 5 10 15

Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val  
 20 25 30  
 Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
 35 40 45  
 Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
 50 55 60  
 Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
 65 70 75  
 Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
 80 85 90  
 Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
 95 100 105  
 Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
 110 115 120  
 Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
 125 130 135  
 Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
 140 145 150  
 Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu  
 155 160 165  
 Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly  
 170 175 180  
 Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala  
 185 190 195  
 Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu  
 200 205 210  
 Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala  
 215 220 225  
 Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu  
 230 235 240  
 Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu  
 245 250 255  
 Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys  
 260 265 270  
 Lys Asp Ser

<210> 507  
 <211> 1700  
 <212> DNA  
 <213> Homo sapiens

<400> 507

gccaggcagg tgggcctcag gaggtgcctc caggcggcca gtgggcctga 50  
ggccccagca agggctaggg tccatctcca gtcccaggac acagcagcgg 100  
ccaccatggc cacgcctggg ctccagcagc atcagagcag cccctgtggt 150  
tggcagcaaa gttcagcttg gctgggcccg ctgtgagggg cttcgcgcta 200  
cgccctgcgg tgtcccaggg gctgaggtct cctcatcttc tccctagcag 250  
tggatgagca acccaacggg ggcccgggga ggggaactgg ccccgaggga 300  
gaggaacccc aaagccacat ctgtagccag gatgagcagt gtgaatccag 350  
gcagcccccga ggaccgggga ggcacaggtg gccccacca cccggaggag 400  
cagctcctgc ccctgtccgg gggatgactg attctcctcc gccaggccac 450  
ccagaggaga aggccacccc gcctggaggc acaggccatg aggggctctc 500  
aggaggtgct gctgatgtgg cttctggtgt tggcagtggg cggcacagag 550  
cacgcctacc ggcccggccg taggggtgtg gctgtccggg ctcacgggga 600  
ccctgtctcc gagtgcgttg tgcagcgtgt gtaccagccc ttcctcacca 650  
cctgcgacgg gcaccgggcc tgcagcacct accgaaccat ctataggacc 700  
gcctaccgcc gcagccctgg gctggcccct gccaggcctc gctacgcgtg 750  
ctgccccggc tggaagagga ccagcgggct tctgggggcc tgtggagcag 800  
caatatgcca gccgccatgc cggaacggag ggagctgtgt ccagcctggc 850  
cgctgccgct gccctgcagg atggcggggt gacacttgc agtcagatgt 900  
ggatgaatgc agtgc tagga ggggcggctg tccccagcgc tgcataaca 950  
ccgccggcag ttactggtgc cagtgttggt aggggcacag cctgtctgca 1000  
gacggtacac tctgtgtgcc caaggagggg cccccaggg tggccccaa 1050  
cccagacagga gtggacagt caatgaagga agaagtgcag aggctgcagt 1100  
ccagggtgga cctgctggag gagaagctgc agctggtgct ggccccactg 1150  
cacagcctgg cctcgcaggc actggagcat gggctcccgg accccggcag 1200  
cctcctggtg cactccttc agcagctcgg ccgcatcgac tccctgagcg 1250  
agcagatttc cttcctggag gagcagctgg ggtcctgctc ctgcaagaaa 1300  
gactcgtgac tgcccagcgc tccaggctgg actgagcccc tcacgccgcc 1350  
ctgcagcccc catgccctg cccaacatgc tgggggtcca gaagccacct 1400  
cggggtgact gagcggaagg ccaggcaggg ccttcctcct cttcctcctc 1450

cccttctctcg ggaggtcccc cagaccttg catgggatgg gctgggatct 1500  
 tctctgtgaa tccacccctg gctaccccca cctgggtac cccaacggca 1550  
 tccaaggcc aggtggaccc tcagctgagg gaaggtacga gctccctgct 1600  
 ggagcctggg acccatggca caggccaggc agcccggagg ctgggtgggg 1650  
 cctcagtggg ggctgctgcc tgacccccag cacaataaaa atgaaacgtg 1700

<210> 508  
 <211> 273  
 <212> PRT  
 <213> Homo sapiens

<400> 508

Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu  
 1 5 10 15

Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val  
 20 25 30

Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
 35 40 45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
 50 55 60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
 65 70 75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
 80 85 90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
 95 100 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
 110 115 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
 125 130 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
 140 145 150

Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu  
 155 160 165

Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly  
 170 175 180

Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala  
 185 190 195

Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu  
 200 205 210

FOOTNOTES: 1802

Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala  
 215 220 225  
 Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu  
 230 235 240  
 Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu  
 245 250 255  
 Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys  
 260 265 270  
 Lys Asp Ser

<210> 509  
 <211> 1538  
 <212> DNA  
 <213> Homo sapiens

<400> 509  
 cccacgcgtc cgaagctggc cctgcacggc tgcaagggag gtcctgtgg 50  
 acagggcagg caggtgggcc tcaggaggtg cctccaggcg gccagtgggc 100  
 ctgaggcccc agcaagggct agggctcatc tccagtcca ggacacagca 150  
 gcggccacca tggccacgcc tgggctccag cagcatcagc agccccagg 200  
 accggggagg cacaggtggc cccaccacc cggaggagca gtcctgccc 250  
 ctgtccgggg gatgactgat tctcctccgc caggccacc agaggagaag 300  
 gccacccgc ctggaggcac aggccatgag gggctctcag gagtgctgc 350  
 tgatgtggct tctggtgttg gcagtgggcg gcacagagca cgcctaccg 400  
 cccggccgta ggggtgtgtc tgtccgggt caccgggacc ctgtctccga 450  
 gtcgttcgtg cagcgtgtgt accagccctt cctcaccacc tgcgacgggc 500  
 accgggcctg cagcacctac cgaaccatct ataggaccgc ctaccgccgc 550  
 agccctgggc tggcccctgc caggcctcgc tacgcgtgct gcccgggctg 600  
 gaagaggacc agcgggcttc ctggggcctg tggagcagca atatgccagc 650  
 cgccatgccg gaacggaggg agctgtgtcc agcctggccg ctgccgctgc 700  
 cctgcaggat ggcggggtga cacttgccag tcagatgtgg atgaatgcag 750  
 tgctaggagg ggcggctgtc cccagcgtg cgtcaacacc gccggcagtt 800  
 actggtgcca gtgttgggag gggcacagcc tgtctgcaga cggtacactc 850  
 tgtgtgcca agggagggcc cccagggtg gcccacaacc cgacaggagt 900  
 ggacagtgca atgaaggaag aagtgcagag gctgcagtcc aggggtggacc 950

tgctggagga gaagctgcag ctggtgctgg cccactgca cagcctggcc 1000  
 tcgcaggcac tggagcatgg gctcccgac cccggcagcc tcctggtgca 1050  
 ctcttccag cagctcggcc gcatcgactc cctgagcgag cagatttcct 1100  
 tcctggagga gcagctgggg tcctgctcct gcaagaaaga ctcgtgactg 1150  
 cccagcgccc caggctggac tgagcccctc acgccgccct gcagcccca 1200  
 tgccctgcc caacatgctg ggggtccaga agccacctcg gggtgactga 1250  
 gcggaaggcc aggcagggcc ttctctctct tcctctctcc cttctcggg 1300  
 aggtcccca gaccctggca tgggatgggc tgggatcttc tctgtgaatc 1350  
 caccctggc taccaccacc ctggctaccc caacggcatc ccaaggccag 1400  
 gtgggccctc agctgagga aggtacgagc tccctgctgg agcctgggac 1450  
 ccatggcaca ggccaggcag cccggaggct ggggtggggc tcagtggggg 1500

ctgtgcctg accccagca caataaaat gaaacgtg 1538

<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu  
1 5 10 15

Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val  
20 25 30

Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
35 40 45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
50 55 60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
65 70 75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
80 85 90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
95 100 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
110 115 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
125 130 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln

140	145	150
Arg Cys Val Asn Thr Ala Gly Ser Tyr	Trp Cys Gln Cys Trp Glu	
155	160	165
Gly His Ser Leu Ser Ala Asp Gly Thr	Leu Cys Val Pro Lys Gly	
170	175	180
Gly Pro Pro Arg Val Ala Pro Asn Pro	Thr Gly Val Asp Ser Ala	
185	190	195
Met Lys Glu Glu Val Gln Arg Leu Gln	Ser Arg Val Asp Leu Leu	
200	205	210
Glu Glu Lys Leu Gln Leu Val Leu Ala	Pro Leu His Ser Leu Ala	
215	220	225
Ser Gln Ala Leu Glu His Gly Leu Pro	Asp Pro Gly Ser Leu Leu	
230	235	240
Val His Ser Phe Gln Gln Leu Gly Arg	Ile Asp Ser Leu Ser Glu	
245	250	255
Gln Ile Ser Phe Leu Glu Glu Gln Leu	Gly Ser Cys Ser Cys Lys	
260	265	270

Lys Asp Ser

<210> 511

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 511

tgagcagca atatgccagc c 21

<210> 512

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 512

ttttccactc ctgtcgggtt gg 22

<210> 513

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe



<400> 513  
ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514  
<211> 2690  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2039-2065  
<223> unknown base

<400> 514  
ggttgccaca gctggtttag ggccccgacc actggggccc cttgtcagga 50  
ggagacagcc tcccggcccg gggaggacaa gtcgctgcca cctttggtg 100  
ccgacgtgat tccctgggac ggtccgtttc ctgccgtcag ctgccggccg 150  
agttgggtct cgtgtttca ggccggtcc ccttctctgg tctccctct 200  
cccgtgggc cgtttatcg ggaggagatt gtcttcagg gctagcaatt 250  
ggacttttga tgatgtttga ccagcggca ggaatagcag gcaacgtgat 300  
ttcaaagctg ggctcagcct ctgtttcttc tctcgtgtaa tcgcaaaacc 350  
cattttggag caggaattcc aatcatgtct gtgatggtg tgagaaagaa 400  
ggtgacacgg aaatgggaga aactcccagg caggaacacc ttttgctgtg 450  
atggccgct catgatggc cggcaaaagg gcattttcta cctgaccctt 500  
ttcctcatcc tggggacatg tacactcttc ttgcctttg agtgccgcta 550  
cctggctgtt cagctgtctc ctgccatccc tgtatttgct gccatgctct 600  
tccttttctc catggctaca ctgttgagga ccagcttcag tgaccctgga 650  
gtgattcttc gggcgtacc agatgaagca gctttcatag aaatggagat 700  
agaagctacc aatggtgcgg tgccccagg ccagcgacca ccgcctcgta 750  
tcaagaattt ccagataaac aaccagattg tgaaactgaa atactgttac 800  
acatgcaaga tcttcggcc tccccgggc tccattgca gcatctgtga 850  
caactgtgtg gagcgttcg accatcactg cccctgggtg gggaattgtg 900  
ttggaaagag gaactaccgc tacttctacc tcttcatcct ttctctctcc 950  
ctctcaciaa tctatgtctt cgccttcaac atcgtctatg tggccctcaa 1000  
atctttgaaa attggcttct tggagacatt gaaagaaact cctggaactg 1050  
ttctagaagt cctcatttgc ttctttacac tctggtccgt cgtgggactg 1100

actggatttc atactttcct cgtggctctc aaccagacaa ccaatgaaga 1150  
 catcaaagga tcatggacag ggaagaatcg cgtccagaat ccctacagcc 1200  
 atggcaatat tgtgaagaac tgctgtgaag tgctgtgtgg ccccttgccc 1250  
 cccagtgtgc tggatcgaag gggatatttg cactggagg aaagtggaag 1300  
 tcgacctccc agtactcaag agaccagtag cagcctcttg ccacagagcc 1350  
 cagccccac agaacacctg aactcaaag agatgccgga ggacagcagc 1400  
 actcccgaag agatgccacc tccagagccc ccagagccac cacaggaggc 1450  
 agctgaagct gagaagtagc ctatctatgg aagagacttt tgtttgtgtt 1500  
 taattagggc tatgagagat ttcaggtgag aagttaaacc tgagacagag 1550  
 agcaagtaag ctgtcccttt taactgtttt tcttttgtct ttagtcaccc 1600  
 agttgcacac tggcattttc ttgctgcaag cttttttaa tttctgaact 1650  
 caaggcagtg gcagaagatg tcagtcacct ctgataactg gaaaaatggg 1700  
 tctcttgggc cctggcactg gttctccatg gcctcagcca cagggtcccc 1750  
 ttggaccccc tctcttcctt ccagatccca gccctcctgc ttggggtcac 1800  
 tgggtctcatt ctggggctaa aagtttttga gactggctca aatcctccca 1850  
 agctgctgca cgtgctgagt ccagaggcag tcacagagac ctctggccag 1900  
 gggatcctaa ctgggttctt ggggtcttca ggactgaaga ggaggagag 1950  
 tggggtcaga agattctcct ggccaccaag tgccagcatt gccacaaat 2000  
 ccttttagga atgggacagg taccttcac ttgttgann nnnnnnnnn 2050  
 nnnnnnnnn nnnnttggt tttcttttg actcctgctc ccattaggag 2100  
 caggaatggc agtaataaaa gtctgcactt tggtcatttc tttctcag 2150  
 aggaagcccg agtgtcact taaacactat cccctcagac tccctgtgtg 2200  
 aggctcgag aggcctgaa tgcacaaatg ggaaaccaag gcacagagag 2250  
 gctctcctct cctctcctct ccccgatgt accctcaaaa aaaaaaaat 2300  
 gctaaccagt tcttcatta agcctcggt gagtgaggga aagcccagca 2350  
 ctgctgccct ctgggtaac tcaccctaag gcctcgccc acctctggct 2400  
 atggtaacca cactgggggc ttctccaag cccgctctt ccagcacttc 2450  
 caccggcaga gtcccagag cacttcaccc tgggggtggg ctgtggcccc 2500  
 cagtcagctc tgctcaggac ctgctctatt tcaggaaga agatttatgt 2550

attatatgtg gctatatttc ctagagcacc tgtgttttcc tctttctaag 2600  
ccagggctct gtctggatga cttatgcggt gggggagtgt aaaccggaac 2650  
ttttcatcta ttggaaggcg attaaactgt gtctaatagca 2690

<210> 515  
<211> 364  
<212> PRT  
<213> Homo sapiens

<400> 515

Met Ser Val Met Val Val Arg Lys Lys Val Thr Arg Lys Trp Glu  
1 5 10 15

Lys Leu Pro Gly Arg Asn Thr Phe Cys Cys Asp Gly Arg Val Met  
20 25 30

Met Ala Arg Gln Lys Gly Ile Phe Tyr Leu Thr Leu Phe Leu Ile  
35 40 45

Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu  
50 55 60

Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu  
65 70 75

Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp  
80 85 90

Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile  
95 100 105

Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln  
110 115 120

Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile  
125 130 135

Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro  
140 145 150

Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe  
155 160 165

Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn  
170 175 180

Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr  
185 190 195

Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser  
200 205 210

Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr  
215 220 225

Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val

FOOTNOTES

230	235	240
Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln Thr		
245	250	255
Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val		
260	265	270
Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu		
275	280	285
Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly		
290	295	300
Ile Leu Pro Leu Glu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln		
305	310	315
Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu		
320	325	330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu		
335	340	345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala		
350	355	360
Glu Ala Glu Lys		

TOP-PROT-4002-FOOT

<210> 516  
 <211> 255  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> unsure  
 <222> 36, 38, 88, 118, 135, 193, 213, 222  
 <223> unknown base

<400> 516  
 aaaaccctgt attttttaca atgcaaata gacaatnanc tggaggtctt 50  
 tgaattaggt attataggga tgggtggggtt gatttttntt cctggaggct 100  
 tttggctttg gactctcnct ttctcccaca gacncttcg accatcactg 150  
 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200  
 tcttcatcct ttntctctcc cncctcacia tctatgtctt cgccttcaac 250  
 atcgt 255

<210> 517  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
 <220>

<223> Synthetic oligonucleotide probe

<400> 517

caacgtgatt tcaaagctgg gctc 24

<210> 518

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

gcctcgatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtgaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520

ctcacctgaa atctctcata gccc 24

<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

cgcaaaaccc attttgggag caggaattcc aatcatgtct gtgatggtgg 50

<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

gttgtgtcct tcagcaaaac agtggattta aatctccttg cacaagcttg 50

agagcaacac aatctatcag gaaagaaaga aagaaaaaaa ccgaacctga 100

caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150  
 aaaaatgcac aattctatct cttgggcaat cttcacggg ctggtgctc 200  
 tgtgtctctt ccaaggagtgc cccgtgcgca gcgagatgc caccttccc 250  
 aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300  
 gtgcactatt gacaaccggg tcacccgggt ggcctggcta aaccgcagca 350  
 ccacctctta tgctgggaat gacaagtggg gcctggatcc tcgctgggtc 400  
 cttctgagca acacccaaac gcagtacagc atcgagatcc agaactgga 450  
 tgtgtatgac gagggccctt acacctgctc ggtgcagaca gacaaccacc 500  
 caaagacctc taggtccac ctcattgtgc aagtatctcc caaaattgta 550  
 gagatttctt cagatatctc cattaatgaa gggaacaata ttagcctcac 600  
 ctgcatagca actggtagac cagagcctac ggttacttgg agacacatct 650  
 ctcccaaagc ggttggtttt gtgagtgaag acgaatactt ggaaattcag 700  
 ggcatcaccg gggagcagtc aggggactac gagtgcagtg cctccaatga 750  
 cgtggccgcg cccgtggtac ggagagtaaa ggtcacctg aactatccac 800  
 catacatttc agaagccaag ggtacagtg tcccgtggg aaaaagggg 850  
 aactgcagtg gtgaagctc agcagctccc tcagcagaat tccagtggta 900  
 caaggatgac aaaagactga ttgaaggaaa gaaagggtg aaagtggaaa 950  
 acagaccttt cctctcaaaa ctcattctt tcaatgtctc tgaacatgac 1000  
 tatgggaact acattgctg ggcctccaac aagctgggac acaccaatgc 1050  
 cagcatcatg ctatttggc caggcgccgt cagcgaggtg agcaacggca 1100  
 cgtcgaggag ggcaggctgc gtctggctgc tgcctcttct ggtcttgac 1150  
 ctgcttctca aattttgatg tgagtgcac ttccccacc gggaaggct 1200  
 gccgccacca ccaccacca cacaacagca atggcaacac cgacagcaac 1250  
 caatcagata tatacaaatg aaattagaag aaacacagcc tcatgggaca 1300  
 gaaatttgag ggagggaac aaagaatact ttggggggaa aagagtttta 1350  
 aaaaagaaat tgaaaattgc cttgcagata ttaggtaca atggagtttt 1400  
 cttttcccaa acgggaagaa cacagcacac ccggttga cccactgcaa 1450  
 gctgcatcgt gcaacctctt tgggtgccagt gtgggcaagg gctcagctc 1500  
 tctgccaca gagtgcctcc acgtggaaca ttctggagct ggccatcca 1550

aattcaatca gtccatagag acgaacagaa tgagaccttc cggcccaagc 1600  
 gtggcgctgc gggcactttg gtagactgtg ccaccacggc gtgtgttg 1650  
 aaacgtgaaa taaaaagagc aaaaaaaaaa 1679

<210> 523  
 <211> 344  
 <212> PRT  
 <213> Homo sapiens

<400> 523

Met Lys Thr Ile Gln Pro Lys Met His Asn Ser Ile Ser Trp Ala  
 1 5 10 15

Ile Phe Thr Gly Leu Ala Ala Leu Cys Leu Phe Gln Gly Val Pro  
 20 25 30

Val Arg Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val  
 35 40 45

Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp  
 50 55 60

Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu  
 65 70 75

Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu  
 80 85 90

Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val  
 95 100 105

Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp  
 110 115 120

Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser  
 125 130 135

Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly  
 140 145 150

Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro  
 155 160 165

Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala Val Gly Phe Val  
 170 175 180

Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln  
 185 190 195

Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro  
 200 205 210

Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile  
 215 220 225

Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr

TEB02T001

230	235	240
Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp		
245	250	255
Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys		
260	265	270
Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val		
275	280	285
Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys		
290	295	300
Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala		
305	310	315
Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val		
320	325	330
Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe		
335	340	

Forward

```

<210> 524
<211> 503
<212> DNA
<213> Homo sapiens

<400> 524
gaaaaaaaaat catgaaaacc atccagccaa aaatgcacaa ttctatctct 50
tgggcaatct tcacggggct ggctgctctg tgtctcttcc aaggagtgcc 100
cgtgcgcagc ggagatgcc ccttcccaa agctatggac aacgtgacgg 150
tccggcaggg ggagagcgcc accctcaggt gcactattga caaccgggtc 200
accggggtgg cctggctaaa ccgcagcacc atctctatg ctgggaatga 250
caagtgggtgc ctggatcctc gcgtggctct tctgagcaac acccaaacgc 300
agtacagcat cgagatccag aacgtggatg tgtatgacga gggcccttac 350
acctgctcgg tgcagacaga caaccaccca aagacctcta gggtcacact 400
cattgtgcaa gtatctccca aaattgtaga gatttcttca gatatctcca 450
ttaatgaagg gaacaatatt agcctcacct gcatagcaac tggtagacca 500
gag 503

```

```

<210> 525
<211> 2602
<212> DNA
<213> Homo sapiens

```

```

<400> 525
atggctggtg acggcggggc cgggcagggg accggggccg cggcccggga 50

```



gcggggccagc tgccggggagc cctgaatcac cgcctggccc gactccacca 100  
 tgaacgtcgc gctgcaggag ctgggagctg gcagcaacgt gggattccag 150  
 aaggggacaa gacagctgtt aggctcacgc acgcagctgg agctgggtctt 200  
 agcaggtgcc tctctactgc tggctgcact gcttctgggc tgccttgttg 250  
 ccctaggggt ccagtaccac agagacccat cccacagcac ctgccttaca 300  
 gaggcctgca ttcgagtggc tggaaaaatc ctggagtccc tggaccgagg 350  
 ggtgagcccc tgtgaggact ttaccagtt ctctgtggg ggctggattc 400  
 ggaggaaccc cctgcccgat gggcgttctc gctggaacac cttcaacagc 450  
 ctctgggacc aaaaccaggc catactgaag cacctgcttg aaaacaccac 500  
 cttcaactcc agcagtgaag ctgagcagaa gacacagcgc ttctacctat 550  
 cttgcctaca ggtggagcgc attgaggagc tgggagccca gccactgaga 600  
 gacctcattg agaagattgg tggttggaac attacggggc cctgggacca 650  
 ggacaacttt atggaggtgt tgaaggcagt agcagggacc tacagggcca 700  
 cccattctt caccgtctac atcagtgccg actctaagag ttccaacagc 750  
 aatgttatcc aggtggacca gtctgggctc tttctgccct ctggggatta 800  
 ctacttaaac agaactgcca atgagaaagt gctcactgcc tatctggatt 850  
 acatggagga actggggatg ctgctgggtg ggcggccac ctccacgagg 900  
 gagcagatgc agcaggtgct ggagttggag atacagctgg ccaacatcac 950  
 agtgcgccag gaccagcggc gcgacgagga gaagatctac cacaagatga 1000  
 gcatttoggg gctgcaggct ctggcgccct ccatggactg gcttgagttc 1050  
 ctgtctttct tgctgtcacc attggagttg agtgactctg agcctgtggt 1100  
 ggtgtatggg atggattatt tgcagcaggt gtcagagctc atcaaccgca 1150  
 cggaccaag catcctgaac aattacctga tctggaacct ggtgcaaaag 1200  
 acaacctcaa gcctggaccg acgctttgag tctgcacaag agaagctgct 1250  
 ggagaccctc tatggcacta agaagtctg tgtgccgagg tggcagacct 1300  
 gcatctcaa cacggatgac gcccttggct ttgctttggg gtcactcttc 1350  
 gtgaaggcca cgtttgaccg gcaaagcaaa gaaattgcag aggggatgat 1400  
 cagcgaaatc cggaccgcat ttgaggaggc cctgggacag ctggtttga 1450  
 tggatgagaa gaccggccag gcagccaagg agaaagcaga tgccatctat 1500

gatatgattg gtttcccaga ctttatcctg gagcccaaag agctggatga 1550  
tgtttatgac gggtagaaa tttctgaaga ttctttcttc caaaacatgt 1600  
tgaatttgta caacttctct gccaaagtta tggctgacca gctccgcaag 1650  
cctcccagcc gagaccagtg gagcatgacc cccagacag tgaatgccta 1700  
ctaccttcca actaagaatg agatcgtctt ccccgctggc atcctgcagg 1750  
cccccttcta tgcccgcaac caccccaagg ccctgaactt cgggtggcatc 1800  
gggtgtggtca tgggccatga gttgacgcat gcctttgatg accaagggcg 1850  
cgagtatgac aaagaaggga acctgcggcc ctggtggcag aatgagtccc 1900  
tggcagcctt ccggaaccac acggcctgca tggaggaaca gtacaatcaa 1950  
taccaggtca atggggagag gctcaacggc cgccagacgc tgggggagaa 2000  
cattactgac aacggggggc tgaaggctgc ctacaatgct tacaagcat 2050  
ggctgagaaa gcatggggag gagcagcaac tgccagccgt ggggctcacc 2100  
aaccaccagc tcttctcgt gggatttgcc cagggtgtgt gctcggtcgg 2150  
cacaccagag agctctcacg aggggctggt gaccgacccc cacagccctg 2200  
cccgcttcgg cgtgctgggc actctctcca actcccgta cttcctgcgg 2250  
cacttcggct gccctgtcgg ctcccccag aaccagggc agctgtgtga 2300  
gggtgtggtag acctggatca ggggagaaat ggccagctgt caccagacct 2350  
ggggcagctc tctgacaaa gctgtttgct cttgggttg gaggaagcaa 2400  
atgcaagctg ggctgggtct agtccctccc cccacaggt gacatgagta 2450  
cagaccctcc tcaatcacca cattgtgcct ctgctttggg ggtgcccctg 2500  
cctccagcag agccccacc attcactgtg acatctttcc gtgtcaccct 2550  
gcctggaaga ggtctgggtg gggaggccag ttcccatagg aaggagtctg 2600  
cc 2602

<210> 526

<211> 736

<212> PRT

<213> Homo sapiens

<400> 526

Met	Asn	Val	Ala	Leu	Gln	Glu	Leu	Gly	Ala	Gly	Ser	Asn	Val	Gly
1				5				10						15

Phe	Gln	Lys	Gly	Thr	Arg	Gln	Leu	Leu	Gly	Ser	Arg	Thr	Gln	Leu
				20					25					30

Glu Leu Val Leu Ala Gly Ala Ser Leu Leu Leu Ala Ala Leu Leu  
 35 40 45  
 Leu Gly Cys Leu Val Ala Leu Gly Val Gln Tyr His Arg Asp Pro  
 50 55 60  
 Ser His Ser Thr Cys Leu Thr Glu Ala Cys Ile Arg Val Ala Gly  
 65 70 75  
 Lys Ile Leu Glu Ser Leu Asp Arg Gly Val Ser Pro Cys Glu Asp  
 80 85 90  
 Phe Tyr Gln Phe Ser Cys Gly Gly Trp Ile Arg Arg Asn Pro Leu  
 95 100 105  
 Pro Asp Gly Arg Ser Arg Trp Asn Thr Phe Asn Ser Leu Trp Asp  
 110 115 120  
 Gln Asn Gln Ala Ile Leu Lys His Leu Leu Glu Asn Thr Thr Phe  
 125 130 135  
 Asn Ser Ser Ser Glu Ala Glu Gln Lys Thr Gln Arg Phe Tyr Leu  
 140 145 150  
 Ser Cys Leu Gln Val Glu Arg Ile Glu Glu Leu Gly Ala Gln Pro  
 155 160 165  
 Leu Arg Asp Leu Ile Glu Lys Ile Gly Gly Trp Asn Ile Thr Gly  
 170 175 180  
 Pro Trp Asp Gln Asp Asn Phe Met Glu Val Leu Lys Ala Val Ala  
 185 190 195  
 Gly Thr Tyr Arg Ala Thr Pro Phe Phe Thr Val Tyr Ile Ser Ala  
 200 205 210  
 Asp Ser Lys Ser Ser Asn Ser Asn Val Ile Gln Val Asp Gln Ser  
 215 220 225  
 Gly Leu Phe Leu Pro Ser Arg Asp Tyr Tyr Leu Asn Arg Thr Ala  
 230 235 240  
 Asn Glu Lys Val Leu Thr Ala Tyr Leu Asp Tyr Met Glu Glu Leu  
 245 250 255  
 Gly Met Leu Leu Gly Gly Arg Pro Thr Ser Thr Arg Glu Gln Met  
 260 265 270  
 Gln Gln Val Leu Glu Leu Glu Ile Gln Leu Ala Asn Ile Thr Val  
 275 280 285  
 Pro Gln Asp Gln Arg Arg Asp Glu Glu Lys Ile Tyr His Lys Met  
 290 295 300  
 Ser Ile Ser Glu Leu Gln Ala Leu Ala Pro Ser Met Asp Trp Leu  
 305 310 315  
 Glu Phe Leu Ser Phe Leu Leu Ser Pro Leu Glu Leu Ser Asp Ser

320	325	330
Glu Pro Val Val Val Tyr Gly Met Asp Tyr Leu Gln Gln Val Ser		
335	340	345
Glu Leu Ile Asn Arg Thr Glu Pro Ser Ile Leu Asn Asn Tyr Leu		
350	355	360
Ile Trp Asn Leu Val Gln Lys Thr Thr Ser Ser Leu Asp Arg Arg		
365	370	375
Phe Glu Ser Ala Gln Glu Lys Leu Leu Glu Thr Leu Tyr Gly Thr		
380	385	390
Lys Lys Ser Cys Val Pro Arg Trp Gln Thr Cys Ile Ser Asn Thr		
395	400	405
Asp Asp Ala Leu Gly Phe Ala Leu Gly Ser Leu Phe Val Lys Ala		
410	415	420
Thr Phe Asp Arg Gln Ser Lys Glu Ile Ala Glu Gly Met Ile Ser		
425	430	435
Glu Ile Arg Thr Ala Phe Glu Glu Ala Leu Gly Gln Leu Val Trp		
440	445	450
Met Asp Glu Lys Thr Arg Gln Ala Ala Lys Glu Lys Ala Asp Ala		
455	460	465
Ile Tyr Asp Met Ile Gly Phe Pro Asp Phe Ile Leu Glu Pro Lys		
470	475	480
Glu Leu Asp Asp Val Tyr Asp Gly Tyr Glu Ile Ser Glu Asp Ser		
485	490	495
Phe Phe Gln Asn Met Leu Asn Leu Tyr Asn Phe Ser Ala Lys Val		
500	505	510
Met Ala Asp Gln Leu Arg Lys Pro Pro Ser Arg Asp Gln Trp Ser		
515	520	525
Met Thr Pro Gln Thr Val Asn Ala Tyr Tyr Leu Pro Thr Lys Asn		
530	535	540
Glu Ile Val Phe Pro Ala Gly Ile Leu Gln Ala Pro Phe Tyr Ala		
545	550	555
Arg Asn His Pro Lys Ala Leu Asn Phe Gly Gly Ile Gly Val Val		
560	565	570
Met Gly His Glu Leu Thr His Ala Phe Asp Asp Gln Gly Arg Glu		
575	580	585
Tyr Asp Lys Glu Gly Asn Leu Arg Pro Trp Trp Gln Asn Glu Ser		
590	595	600
Leu Ala Ala Phe Arg Asn His Thr Ala Cys Met Glu Glu Gln Tyr		
605	610	615

Asn	Gln	Tyr	Gln	Val	Asn	Gly	Glu	Arg	Leu	Asn	Gly	Arg	Gln	Thr	
				620					625					630	
Leu	Gly	Glu	Asn	Ile	Thr	Asp	Asn	Gly	Gly	Leu	Lys	Ala	Ala	Tyr	
				635					640					645	
Asn	Ala	Tyr	Lys	Ala	Trp	Leu	Arg	Lys	His	Gly	Glu	Glu	Gln	Gln	
				650					655					660	
Leu	Pro	Ala	Val	Gly	Leu	Thr	Asn	His	Gln	Leu	Phe	Phe	Val	Gly	
				665					670					675	
Phe	Ala	Gln	Val	Trp	Cys	Ser	Val	Arg	Thr	Pro	Glu	Ser	Ser	His	
				680					685					690	
Glu	Gly	Leu	Val	Thr	Asp	Pro	His	Ser	Pro	Ala	Arg	Phe	Arg	Val	
				695					700					705	
Leu	Gly	Thr	Leu	Ser	Asn	Ser	Arg	Asp	Phe	Leu	Arg	His	Phe	Gly	
				710					715					720	
Cys	Pro	Val	Gly	Ser	Pro	Met	Asn	Pro	Gly	Gln	Leu	Cys	Glu	Val	
				725					730					735	

Trp

<210> 527  
 <211> 4308  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> unsure  
 <222> 1478, 3978, 4057-4058, 4070  
 <223> unknown base

<400> 527  
 gcccgccct cgcgcctcgc cactcccgcc tccctccctc cgcccgctcc 50  
 cgcgcctcc tccctccctc ctccccagct gtcccggtcg cgtcatgccc 100  
 agcctcccg ccccgccggc cccgctgctg ctctcgggc tgctgctgct 150  
 cggtcccg cggcccgcg gcgcggccc agagcccccc gtgtgccc 200  
 tccgttctga gaaggagccg ctgcccgttc ggggagcggc aggtaggtgg 250  
 gcgcccggg gaggcgcgg cggggagtcg ggctcggggc ggtcagcgc 300  
 cagcccgag ggggcgcgg gcgcaggtgg ctgggcgcgg cgggcggccc 350  
 ggaggggtgg cgggggcaga agggcgcggt gcctgggacc cgggacccgc 400  
 gggcagcccc cggggcgga cacggcgga gctgggcagc ggcctccagc 450  
 caagcccgtc cccgcaggt gcaccttcgg cggaaggtc tatgccttgg 500

acgagacgtg gcacccggac ctaggggagc cattcggggt gatgcgctgc 550  
 gtgctgtgcg cctgcgaggc gcagtggggt cgccgtacca ggggccctgg 600  
 cagggtcagc tgcaagaaca tcaaaccaga gtgccaacc ccggcctgtg 650  
 ggcagccgcg ccagctgccg ggacactgct gccagacctg cccccaggac 700  
 ttcgtggcgc tgetgacagg gccgaggtcg caggcgggtg cacgagcccg 750  
 agtctcgctg ctgcgtctta gcctccgctt ctctatctcc tacaggcggc 800  
 tggaccgcc taccaggatc cgcttctcag actccaatgg cagtgtcctg 850  
 tttgagcacc ctgcagcccc cacccaagat ggcctggtct gtggggtgtg 900  
 gggggcagtg cctcggttgt ctctgcggct ccttagggca gaacagctgc 950  
 ----- atgtggcact tgtgacactc actcacctt caggggaggt ctgggggcct 1000  
 ctcatccggc accgggccct gtcccagag accttcagt ccatoctgac 1050  
 tctagaaggc ccccaccagc agggcgtagg gggcatcacc ctgctcactc 1100  
 tcagtgcacac agaggactcc ttgcattttt tgctgtcttt ccgaggcctt 1150  
 gcaggactaa cccaggttcc cttgaggctc cagattctac accaggggca 1200  
 gctactgcga gaacttcagg ccaatgtctc agcccaggaa ccaggctttg 1250  
 ctgaggtgct gccaacctg acagtccagg agatggactg gctggtgctg 1300  
 ggggagctgc agatggccct ggagtgggca ggcaggccag ggctgcgcat 1350  
 cagtggacac attgtgccca ggaagagctg cgacgtcctg caaagtgtcc 1400  
 tttgtggggc taatgcctg atcccagtc aaacgggtgc tgccggctca 1450  
 gccagcctca ctctgctagg aaatggcnc ctagtcctcc aggtgcaatt 1500  
 ggtagggaca accagtgagg tgggtggcat gacactggaa accaagcctc 1550  
 agcggaggga tcagcccact gtctgtgcc acatggctgg cctatcctcc 1600  
 cctgccccca ggccgtgggt atctgccctg ggctggggtg cccgaggggc 1650  
 tcatatgctg ctgcagaatg agctcttcct gaacgtgggc accaaggact 1700  
 tcccagacgg agagcttcgg gggcaacgtg gctgccctgc cctactgtgg 1750  
 ggcatagcgc ccgccctgcc cgtgcccta gcaggagccc tgggtgtacc 1800  
 ccctgtgaag agccaagcag cagggcacgc ctggctttcc ttggataccc 1850  
 actgtcacct gcactatgaa gtgctgctgg ctgggcttgg tggtcagaa 1900  
 caaggcactg tcaactgcca cctccttggg cctcctggaa cgccagggcc 1950



gcctctccac tccctctccc ctctccaac attccctccc ttctgtctcc 3450  
 agcagcccca gagaccagaa ctgatccaga gctggagaaa gaagccgaag 3500  
 gctcttaggg agcagccaga gggccaagtg accaagagga tggggcctga 3550  
 gctggggaag ggggtggcatc gaggaccttc ttgcattctc ctgtgggaag 3600  
 cccagtgcct ttgctcctct gtctgcctc tactcccacc cccactacct 3650  
 ctgggaacca cagctccaca agggggagag gcagctgggc cagaccgagg 3700  
 tcacagccac tccaagtccg gccctgccac cctcggcctc tgtcctggaa 3750  
 gcccacccc tttcttctg tacataatgt cactggcttg ttgggatttt 3800  
 taatttatct tcaactcagca ccaagggcc cggacactcc actcctgctg 3850  
 cccctgagct gagcagagtc attattggag agttttgtat ttattaaaac 3900  
 atttcttttt cagtctttgg gcatgaggtt ggctctttgt ggccaggaac 3950  
 ctgagtgggg cctggtggag aaggggnga gagtaggagg tgagagagag 4000  
 gagctctgac acttggggag ctgaaagaga cctggagagg cagaggatag 4050  
 cgtggcnntt ggctggcatn cctgggttcc gcagaggggc tggggatggt 4100  
 tcttgagatg gtctagagac tcaagaattt aggaagtag aagcaggatt 4150  
 ttgactcaag tttagtttcc cacatcgctg gcctgtttgc tgacttcattg 4200  
 tttgaagtgt ctccagagag agaataaaag gtgtcaccag cccctctctc 4250  
 cctccttccc ttcccttccc tttctttccc tcccctccc tcccctccc 4300  
 tcccctcc 4308

TC210-1802.F001

<210> 528  
 <211> 1285  
 <212> DNA  
 <213> Homo sapiens

<400> 528  
 ggccgagcgg ggggtgctgcg cggcgccggt gatggctggt gacggcgggg 50  
 ccgggcaggg gaccggggcc gcggcccggg agcgggccag ctgccgggag 100  
 ccctgaatca ccgctggcc cgactccacc atgaacgtcg cgctgcagga 150  
 gctgggagct ggcagcaacg tgggattcca gaaggggaca agacagctgt 200  
 taggctcacg cagcagctg gagctgggtct tagcagggtc ctctctactg 250  
 ctggctgcac tgcttctggg ctgccttggt gccctagggg tccagtacca 300  
 cagagaccca tcccacagca cctgccttac agaggcctgc attcagtggt 350



ctggaaaaat cctggagtcc ctggaccgag gggtagagccc ctgtgaggac 400  
 ttttaccagt tctcctgtgg gggctggatt cggaggaacc ccctgcccga 450  
 tgggcgttct cgctggaaca ccttcaacag cctctgggac caaaaccagg 500  
 ccatactgaa gcacctgctt gaaaacacca ccttcaactc cagcagtga 550  
 gctgagcaga agacacagcg cttctaccta tcttgccctac aggtggagcg 600  
 cattgaggag ctgggagccc agccactgag agacctcatt gagaagattg 650  
 gtggttgaa cattacgggg ccctgggacc aggacaactt tatggaggtg 700  
 ttgaaggcag tagcagggac ctacagggcc accccattct tcaccgtcta 750  
 catcagtgcc gactctaaga gttccaacag caatgttata caggtggacc 800  
 agtctgggct ctttctgccc tctcgggatt actacttaaa cagaactgcc 850  
 aatgagaaag taaggaacat cttccgaacc cccatcccta cccctggctg 900  
 agctgggctg atccctgttg acttttcctt ttgccaaggg tcagagcagg 950  
 gaaggtagac ctatcctgtc acctagtga caaactgccc ctcccttctt 1000  
 tcttcttttc ttctccctc cctcccttct ttcccctttt ccttccttcc 1050  
 ttctcttat tcttctagta ggtttcatag acacctactg tgtgccagg 1100  
 ccagtggggg aattcggaga tataagtttc cgagccattg ccacaggaag 1150  
 cgttcagtgt cgatgggttc atggacctag ataggctgat aacaaagctc 1200  
 acaagagggt cctgaggatt caggagagac ttatggagcc agcaaagtct 1250  
 tcctgaagag attgcatttg agccagggtc tgtag 1285

T  
D  
T  
E  
D  
T  
= 1802TDDT

<210> 529  
 <211> 1380  
 <212> DNA  
 <213> Homo sapiens

<400> 529  
 atgcctacta ccttccaact aagaatgaga tcgtcttccc cgctggcacc 50  
 ctgcaggccc ccttctatgc ccgcaaccac cccaaggccc tgaacttcgg 100  
 tggcatcggg gtggtcatgg gccatgagtt gacgcattgc tttgatgacc 150  
 aagggcgcga gtatgacaaa gaagggaacc tgcggccctg gtggcagaat 200  
 gagtccctgg cagccttccg gaaccacacg gcctgcatgg aggaacagta 250  
 caatcaatac caggtaaatg gggagaggct caacggccgc cagacgttg 300  
 gggagaacat tgctgacaac ggggggctga aggtgccta caatgcttac 350

aaagcatggc tgagaaagca tggggaggag cagcaactgc cagccgtggg 400  
 gctcaccaac caccagctct tcttcgtggg atttgcacag gtgtggtgct 450  
 cgggtccgcac accagagagc tctcacgagg ggctggtgac cgacccccac 500  
 agccctgccc gcttcgcgt gctgggcact ctctccaact cccgtgactt 550  
 cctgcggcac ttcggtgccc ctgtcggctc ccccatgaac ccagggcagc 600  
 tgtgtgaggt gtggtagacc tggatcaggg gagaaatggc cagctgtcac 650  
 cagacctggg gcagctctcc tgacaaagct gtttgctctt gggttgggag 700  
 gaagcaaagc caagctgggc tgggtctagt ccctccccc cacaggtgac 750  
 atgagtacag accctcctca atcaccacat tgtgcctctg ctttgggggt 800  
 gcccctgcct ccagcagagc cccaccatt cactgtgaca tctttccgtg 850  
 tcaccctgcc tggagaggt ctgggtgggg aggcagttc ccataggaag 900  
 gagtctgctt cttctgtccc caggctcact cagcctggcg gccatggggc 950  
 ctgccgtgcc tgcccactg tgaccacag gcctgggtgg tgtacctcct 1000  
 ggacttctcc ccaggctcac tcagtgcga cttaggggtg gactcagctc 1050  
 tgtctggctc accctcacgg gctaccccca cctcacctg tgetccttgt 1100  
 gccactgctc ccagtgtgc tgctgacctt cactgacagc tcctagtggg 1150  
 agcccaaggg cctctgaaag cctcctgctg cccactgttt ccctgggctg 1200  
 agaggggaag tgcataatgt tagcgggtac tggttcctgt gtcttagggc 1250  
 acaagcctta gcaaatgatt gattctccct ggacaaagca ggaaagcaga 1300  
 tagagcaggg aaaaggaaga acagagttta tttttacaga aaagagggtg 1350  
 ggagggtgtg gtcttgccc ttataggacc 1380

<210> 530

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 530

gaagcagtc agccagcagt agagaggcac ctgctaaga 39

<210> 531

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 531  
 acgcagctgg agctggtctt agca 24  
  
 <210> 532  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 532  
 ggtactggac ccctagggcc acaa 24  
  
 <210> 533  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 533  
 cctcccagcc gagaccagt g 21  
  
 <210> 534  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 534  
 ggtcctataa gggccaagac c 21  
  
 <210> 535  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 535  
 gactagttct agatcgcgag cggccgccct ttttttttt tttt 44  
  
 <210> 536  
 <211> 16  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 536  
cggacgcgtg ggtcga 16

<210> 537  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 537  
cggccgtgat ggctgtgac g 21

<210> 538  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 538  
ggcagactcc ttcctatggg 20

<210> 539  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 539  
ggcacttcat ggtccttgaa a 21

<210> 540  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 540  
cggatgtgtg tgaggccatg cc 22

<210> 541  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 541  
gaaagtaacc acggaggtca agat 24

<210> 542  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 542  
cctcctccga gactgaaagc t 21

<210> 543  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 543  
tcgcgttgct ttttctcgcg tg 22

sequence = 1802-1807  
<210> 544  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 544  
gcgtgcgtca ggttcca 17

<210> 545  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 545  
cgttcgtgca gcgtgtgta 19

<210> 546  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 546  
cttcctcacc acctgcgacg gg 22

<210> 547  
<211> 23  
<212> DNA

<213> Artificial Sequence  
<220>  
<223> Synthetic oligonucleotide probe

<400> 547  
ggtaggcggt cctatagatg gtt 23

<210> 548  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 548  
agatgtggat gaatgcagtg cta 23

<210> 549  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 549  
atcaacaccg ccggcagtta ctgg 24

<210> 550  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 550  
acagagtgtta ccgtctgcag aca 23

<210> 551  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 551  
agcctcctgg tgcactcct 19

<210> 552  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>

```

<223> Synthetic oligonucleotide probe

<400> 552
cgactccctg agcgagcaga ttcc 25

<210> 553
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 553
gctgggcagt cagcagtctt 20

<210> 554
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 554
aatcctccat ctcagatctt ccag 24

<210> 555
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 555
cctcagcggg aacagccggc c 21

<210> 556
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 556
tgggccaagg gctgc 15

<210> 557
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 557

```

tggtggataa ccaacaagat gg 22

<210> 558

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 558

gagtcgcat ccacaccact cttaaagttc tcaa 34

<210> 559

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 559

caggtgctct tttcagtcac gttt 24

<210> 560

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 560

tggccattct caggacaaga g 21

<210> 561

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide probe

<400> 561

cagttaatgcc atttgccctgc ctgcat 26

<210> 562

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 562

tgcttggaat cacatgaca 19

<210> 563



<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthetic oligonucleotide probe

<400> 563  
tgtggcacag acccaatcct 20

<210> 564  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 564  
gaccctgaag gcctccggcc t 21

<210> 565  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 565  
gagagaggga aggcagctat gtc 23

<210> 566  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 566  
cagcccctct ctttcacctg t 21

<210> 567  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 567  
ccatcctgtg cagctgacac acagc 25

<210> 568  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 568  
 gccaggctat gaggtcctt 20  
  
 <210> 569  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 569  
 ttcaagttcc tgaagccgat tat 23  
  
 <210> 570  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 570  
 ccaacttccc tccccagtgc cct 23  
  
 <210> 571  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 571  
 ttggggaagg tagaatttcc ttgtat 26  
  
 <210> 572  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 572  
 cccttctgcc tccaattct 20  
  
 <210> 573  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe

<400> 573  
tctcctccgt ccccttcctc cact 24

<210> 574  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 574  
tgagccactg ccttgcat 20

<210> 575  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 575  
tctgcagacg cgatggataa 20

<210> 576  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 576  
ccgaaaataa aacatcgccc cttctg 26

<210> 577  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 577  
cacgtggcct ttcacactga 20

<210> 578  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 578  
acttgtgaca gcagtatgct gtctt 25

<210> 579  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 579  
aagcttctgt tcaatcccag cgggcc 26

<210> 580  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 580  
atgcacaggg tttttctggt aa 22

THESE ARE THE SEQUENCES  
<210> 581  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 581  
gcaggaaacc ttcgaatctg ag 22

<210> 582  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 582  
acacctgagg cacctgagag aggaactct 29

<210> 583  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 583  
gacagcccag tacacctgca a 21

<210> 584  
<211> 21  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 584

gacggctgga tctgtgagaa a 21

<210> 585

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 585

cacaactgct gaccccgccc a 21

<210> 586

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 586

ccaggatagc acatgctgca 20

<210> 587

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 587

aaactccaac ctgtatcaga tgca 24

<210> 588

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 588

cccccaagcc cttagactct aagcc 25

<210> 589

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 589

gacccggcac cttgctaac 19

<210> 590

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 590

ggacggtcag tcaggatgac a 21

<210> 591

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 591

ttcggcatca tctcttcct ctccc 25

<210> 592

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 592

acaaaaaaaa gggaacaaaa tacga 25

<210> 593

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 593

ctttgaatag aagacttctg gacaattt 28

<210> 594

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 594

TOPI2017-03-01

ttgcaactgg gaatatacca cgacatgaga 30

<210> 595

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 595

tagggtgcta atttgctga taacct 26

<210> 596

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 596

ggctctgagt ctctgcttga 20

<210> 597

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 597

tccaacaacc atttcctct ggtcc 25

<210> 598

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 598

aagcagtagc cattaacaag tca 23

<210> 599

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 599

caagcgtcca gggtttattga 20

<210> 600

<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe

<400> 600  
gactacaagg cgctcagcta 20

<210> 601  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 601  
ccggctgggt ctcaactctc c 21

<210> 602  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 602  
cgttcgtgca gcgtgtgta 19

<210> 603  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 603  
cttcctcacc acctgcgacg gg 22

<210> 604  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 604  
ggtaggcggt cctatagatg gtt 23

<210> 605  
<211> 23  
<212> DNA  
<213> Artificial Sequence



<220>  
<223> Synthetic oligonucleotide probe

<400> 605  
agatgtggat gaatgcagtg cta 23

<210> 606  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 606  
atcaacaccg ccggcagtta ctgg 24

<210> 607  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 607  
acagagtgtta ccgtctgcag aca 23

<210> 608  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 608  
agcctcctgg tgcactcct 19

<210> 609  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 609  
cgactccctg agcgagcaga ttccc 25

<210> 610  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 610  
gctgggcagt cacgagtctt 20

<210> 611  
<211> 2840  
<212> DNA  
<213> Homo Sapien

<400> 611  
cccacgcgtc cgagccgccc gagaattaga cacactccgg acgcgcccaa 50  
aagcaaccga gaggagggga ggcaaaaaca ccgaaaaaca aaaagagaga 100  
aacaacaccc aacaactggg gtggggggaa gaaagaaaga aaagaaaccc 150  
acccacccac caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaatc 200  
ctgtggcgcg ccgcctgggt cccgggaaga ctgccagca ccagggggtg 250  
ggggagtgcg agctgaaagc tgctggagag tgagcagccc tagcagggat 300  
ggacatgatg ctgttggtgc agggtgcttg ttgctcgaa cagtggcttg 350  
cggcgggtgct cctcagcctg tgctgcctgc taccctcctg cctcccggct 400  
ggacagagtg tggacttccc ctgggcggcc gtggacaaca tgatggtcag 450  
aaaaggggac acggcgggtg ttaggtgtta tttggaagat ggagcttcaa 500  
agggtgctg gctgaaccgg tcaagtatta tttttgcggg aggtgataag 550  
tggtcagtgg atcctcgagt ttcaatttca acattgaata aaagggacta 600  
cagcctccag atacagaatg tagatgtgac agatgatggc ccatacacgt 650  
gttctgttca gactcaacat acaccagaa caatgcaggt gcatctaact 700  
gtgcaagttc ctctaaagat atatgacatc tcaaagata tgaccgtcaa 750  
tgaaggaacc aacgtcactc ttacttgttt ggccactggg aaaccagagc 800  
cttccatttc ttggcgacac atctcccat cagcaaaacc atttgaaaat 850  
ggacaatatt tggacattta tggaattaca agggaccagg ctggggaata 900  
tgaatgcagt gcggaaaatg ctgtgtcatt ccagatgtg aggaaagtaa 950  
aagttgttgt caactttgct cctactattc aggaaattaa atctggcacc 1000  
gtgacccccg gacgcagtgg cctgataaga tgtgaagggt caggtgtgcc 1050  
gcctccagcc tttgaatggt acaaaggaga gaagaagctc ttcaatggcc 1100  
aacaaggaat tattattcaa aatttttagca caagatccat tctcactgtt 1150  
accaacgtga cacaggagca cttcggcaat tatacctgtg tggctgcaa 1200  
caagctaggc acaaccaatg cgagcctgcc tcttaaccct ccaagtacag 1250

cccagtatgg aattaccggg agcgtgatg ttcttttctc ctgctggtac 1300  
 cttgtgttga cactgtcctc tttcaccagc atattctacc tgaagaatgc 1350  
 cattctacaa taaattcaaa gaccataaa aggcttttaa ggattctctg 1400  
 aaagtgtga tggtggatc caatctgga cagtttgta aaagcagcgt 1450  
 gggatataat cagcagtgc tacatgggga tgatgcctt ctgtagaatt 1500  
 gtcattatg taaatacttt aattctactc ttttttgatt agctacatta 1550  
 ccttgtgaag cagtacacat tgccttttt ttaagacgtg aaagctctga 1600  
 aattactttt agaggatatt aattgtgatt tcatgtttgt aatctacaac 1650  
 ttttcaaaag cattcagtca tggctctgcta gggtgcaggc tgtagtttac 1700  
 aaaaacgaat attgcagtga atatgtgatt ctttaaggct gcaatacaag 1750  
 cattcagttc cctgtttcaa taagagtcaa tccacattta caaagatgca 1800  
 tttttttctt ttttgataaa aaagcaaata atattgcctt cagattattt 1850  
 cttcaaaata taacacatat ctagattttt ctgcttgcac gatattcagg 1900  
 tttcaggaat gagccttgta atataactgg ctgtgcagct ctgcttctct 1950  
 ttctgtgaag ttcagcatgg gtgtgccttc atacaataat atttttctct 2000  
 ttgtctcaa ctaataaaa atgttttgct aaatcttaca atttgaaagt 2050  
 aaaaataaac cagagtgatc aagttaaacc atacactatc tctaagtaac 2100  
 gaaggagcta ttggactgta aaaatctctt cctgcactga caatgggggt 2150  
 tgagaatttt gccccacact aactcagttc ttgtgatgag agacaattta 2200  
 ataacagtat agtaaata ccatatgatt tctttagttag tagctaaatg 2250  
 ttagatccac cgtgggaaat cattcccttt aaaatgacag cacagtccac 2300  
 tcaaaggatt gcctagcaat acagcatctt ttcctttcac tagtccaagc 2350  
 caaaaatttt aagatgattt gtcagaaagg gcacaaagtc ctatcaccta 2400  
 atattacaag agttggtaag cgctcatcat taattttatt ttgtggcagg 2450  
 tattatgaca gtcgacctgg aggttatgga tatggatatg gacgttccag 2500  
 agactataat ggcagaaacc aggttggtta tgaccgtac tcaggaggaa 2550  
 attacagaga caattatgac aactgaaatg agacatgcac ataatataga 2600  
 tacacaagga ataatttctg atccaggatc gtccttccaa atggctgtat 2650  
 ttataaagggt ttttgagct gcaactgaagc atcttatttt atagtatatc 2700

aaccttttgt ttttaaattg acctgccaag gtagctgaag accttttaga 2750  
cagttccatc ttttttttta aattttttct gcctatttaa agacaaatta 2800  
tgggacgttt gtcaaaaaaa aaaaaaaaaa aaaaaaaaaa 2840

<210> 612  
<211> 352  
<212> PRT  
<213> Homo Sapien

<400> 612

Met Met Leu Leu Val Gln Gly Ala Cys Cys Ser Asn Gln Trp Leu  
1 5 10 15

Ala Ala Val Leu Leu Ser Leu Cys Cys Leu Leu Pro Ser Cys Leu  
20 25 30

Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val Asp Asn  
35 40 45

Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu  
50 55 60

Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile  
65 70 75

Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser  
80 85 90

Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn  
95 100 105

Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr  
110 115 120

Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val Gln Val  
125 130 135

Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu  
140 145 150

Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu  
155 160 165

Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe  
170 175 180

Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln  
185 190 195

Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro  
200 205 210

Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile  
215 220 225

Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu

TOHOUT-1804F001

230	235	240
Ile Arg Cys Glu Gly Ala Gly Val Pro	Pro Pro Ala Phe Glu Trp	
245	250	255
Tyr Lys Gly Glu Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile Ile	
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn Val	
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys	
290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr	
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys	
320	325	330
Trp Tyr Leu Val Leu Thr Leu Ser Ser	Phe Thr Ser Ile Phe Tyr	
335	340	345
Leu Lys Asn Ala Ile Leu Gln		
350		

<210> 613  
 <211> 1797  
 <212> DNA  
 <213> Homo Sapien

<400> 613  
 agtgggtcga tgggaaggat cttctccaa gtggttcctc ttgaggggag 50  
 cattttctgct ggctccagga ctttgccat ctataaagct tggcaatgag 100  
 aaataagaaa attctcaagg aggacgagct cttgagttag acccaacaag 150  
 ctgcttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200  
 cccaagagga gaaatggggt gaacttctcc ctagctgtgg tggatcatcta 250  
 cctgatcctg ctacccgctg gcgctgggct gctgggtggtc caagttctga 300  
 atctgcaggc gcggctccgg gtcttgaga tgtatttctc caatgacact 350  
 ctggcgggctg aggacagccc gtccttctcc ttgctgcagt cagcacaccc 400  
 tggagaacac ctggctcagg gtgcatcgag gctgcaagtc ctgcaggccc 450  
 aactcacctg ggtccgcgtc agccatgagc acttgctgca gcgggtagac 500  
 aacttcactc agaaccagg gatgttcaga atcaaagggtg aacaaggcgc 550  
 cccaggtctt caaggtcaca agggggccat gggcatgcct ggtgcccttg 600  
 gcccgcggg accacctgct gagaaggag ccaagggggc tatgggacga 650

gatggagcaa caggcccctc gggaccccaa ggcccaccgg gagtcaaggg 700  
agaggcgggc ctccaaggac cccaggggtgc tccaggggaag caaggagcca 750  
ctggcaccac aggaccccaa ggagagaagg gcagcaaagg cgatgggggt 800  
ctcattggcc caaaagggga aactggaact aaggagagaga aaggagacct 850  
gggtctccca ggaagcaaag gggacagggg catgaaagga gatgcagggg 900  
tcatggggcc tcttgagacc caggggagta aaggtgactt cgggaggcca 950  
ggcccaccag gtttggtctg ttttcttga gctaaaggag atcaaggaca 1000  
acctggactg caggggtgtt cgggccctcc tgggtgcagt ggacaccag 1050  
gtgccaaggg tgagcctggc agtgctggct cccctgggag agcaggactt 1100  
ccagggagcc ccgggagtcc aggagccaca ggcctgaaag gaagcaaagg 1150  
ggacacagga cttcaaggac agcaaggaag aaaaggagaa tcaggagtcc 1200  
caggccctgc aggtgtgaag ggagaacagg ggagcccagg gctggcaggt 1250  
cccaagggag cccctggaca agctggccag aaggagagacc agggagtga 1300  
aggatcttct ggggagcaag gagtaaaggg agaaaaagg gaaagaggtg 1350  
aaaactcagt gtccgtcagg attgtcggca gtagtaaccg aggccgggct 1400  
gaagtttact acagtggtag ctgggggaca atttgcatg acgagtggca 1450  
aaattctgat gccattgtct tctgccgat gctgggttac tccaaaggaa 1500  
gggccctgta caaagtggga gctggcactg ggcagatctg gctggataat 1550  
gttcagtgtc ggggcacgga gaggaccctg tggagctgca ccaagaatag 1600  
ctggggccat catgactgca gccacgagga ggacgcaggc gtggagtgca 1650  
gcgtctgacc cggaaccct ttcattctc tgctcccgag gtgtcctcgg 1700  
gctcatatgt gggaaggcag aggatctctg aggagttccc tggggacaac 1750  
tgagcagcct ctggagaggg gccattaata aagctcaaca tcattga 1797

<210> 614  
<211> 520  
<212> PRT  
<213> Homo Sapien

<400> 614  
Met Arg Asn Lys Lys Ile Leu Lys Glu Asp Glu Leu Leu Ser Glu  
1 5 10 15  
Thr Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu  
20 25 30

FOH20T-1802T00T

Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	35	40	45
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	50	55	60
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	140	145	150
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	155	160	165
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	170	175	180
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln	185	190	195
Gly	Pro	Pro	Gly	Val	Lys	Gly	Glu	Ala	Gly	Leu	Gln	Gly	Pro	Gln	200	205	210
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln	215	220	225
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys	230	235	240
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro	245	250	255
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met	260	265	270
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro	275	280	285
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln	290	295	300
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val	305	310	315
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro			





cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350  
 gatgtgagat gatctgttac tgcaacttca gcgaattgct ctgctgcccc 400  
 aaagacgttt tctttggacc aaagatctct ttcgtgattc cttgcaacaa 450  
 tcaatgagaa tcttcatgta ttctggagaa caccattcct gatttccac 500  
 aaactgcact acatcagtat aactgcattt ctagtttcta tatagtgcaa 550  
 tagagcatag attctataaa ttcttacttg tctaagacaa gtaaatctgt 600  
 gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaaa 647

<210> 616  
 <211> 98  
 <212> PRT  
 <213> Homo Sapien

<400> 616

Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu  
 1 5 10 15  
 Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg  
 20 25 30  
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val  
 35 40 45  
 Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp  
 50 55 60  
 Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu  
 65 70 75  
 Leu Leu Cys Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser  
 80 85 90  
 Phe Val Ile Pro Cys Asn Asn Gln  
 95

<210> 617  
 <211> 2558  
 <212> DNA  
 <213> Homo Sapien

<400> 617

cccacgcgtc cgcggacgcg tgggctggac ccaggtctg gagcgaattc 50  
 cagcctgcag ggctgataag cgaggcatta gtgagattga gagagacttt 100  
 accccgccgt ggtggttgga gggcgcgag tagagcagca gcacaggcgc 150  
 gggccccggg aggccggctc tgctcgcgcc gagatgtgga atctccttca 200  
 cgaaccgcac tcggctgtgg ccaccgcgcg ccgccgcgcg tggctgtgcg 250  
 ctggggcgct ggtgctggcg ggtggcttct ttctcctcgg cttcctcttc 300

ggggtggttta taaaatcctc caatgaagct actaacatta ctccaaagca 350  
 taatatgaaa gcatttttgg atgaattgaa agctgagaac atcaagaagt 400  
 tcttacataa ttttacacag ataccacatt tagcaggaac agaacaaaac 450  
 tttcagcttg caaagcaaat tcaatcccag tggaaagaat ttggcctgga 500  
 ttctgttgag ctagctcatt atgatgtcct gttgtcctac ccaaataaga 550  
 ctcatcccaa ctacatctca ataattaatg aagatggaaa tgagattttc 600  
 aacacatcat tatttgaacc acctcctcca ggatatgaaa atgtttcgga 650  
 tattgtacca cttttcagtg ctttctctcc tcaaggaatg ccagagggcg 700  
 atctagtgtg tgtaactat gcacgaactg aagacttctt taaattggaa 750  
 cgggacatga aaatcaattg ctctgggaaa attgtaattg ccagatatgg 800  
 gaaagttttc agaggaaata aggttaaaaa tgcccagctg gcaggggcca 850  
 aaggagtcac tctctactcc gaccctgctg actactttgc tctgggggtg 900  
 aagtcctatc cagacggttg gaatcttctt ggaggtggtg tccagcgtgg 950  
 aaatatccta aatctgaatg gtgcaggaga cctctcaca ccaggttacc 1000  
 cagcaaatga atatgcttat aggcgtggaa ttgcagaggc tgttggtctt 1050  
 ccaagtattc ctgttcatcc aattggatac tatgatgcac agaagctcct 1100  
 agaaaaaatg ggtggctcag caccaccaga tagcagctgg agaggaagtc 1150  
 tcaaagtgcc ctacaatgtt ggacctggct ttactggaaa cttttctaca 1200  
 caaaaagtca agatgcacat ccactctacc aatgaagtga cgagaattta 1250  
 caatgtgata ggtactctca gaggagcagt ggaaccagac agatatgtca 1300  
 ttctgggagg tcaccgggac tcatgggtgt ttggtggtat tgaccctcag 1350  
 agtggagcag ctgttggtca tgaaatttg aggagctttg gaacactgaa 1400  
 aaaggaaggg tggagaccta gaagaacaat tttgtttgca agctgggatg 1450  
 cagaagaatt tggcttctt ggttctactg agtgggcaga ggagaattca 1500  
 agactccttc aagagcgtgg cgtggcttat attaagtctg actcatctat 1550  
 agaaggaaac tacactctga gagttgattg tacaccgctg atgtacagct 1600  
 tggtagacaa cctaacaaaa gagctgaaaa gccctgatga aggctttgaa 1650  
 ggcaaatctc tttatgaaag ttggactaaa aaaagtcctt ccccagagtt 1700  
 cagtggcatg cccaggataa gcaaattggg atctggaaat gattttgagg 1750



10017084-102404

Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu		95	100	105
Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro		110	115	120
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly		125	130	135
Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly		140	145	150
Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser		155	160	165
Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala		170	175	180
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn		185	190	195
Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg		200	205	210
Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Val		215	220	225
Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys		230	235	240
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg		245	250	255
Gly	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro		260	265	270
Gly	Tyr	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu		275	280	285
Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr		290	295	300
Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro		305	310	315
Asp	Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly		320	325	330
Pro	Gly	Phe	Thr	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His		335	340	345
Ile	His	Ser	Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly		350	355	360
Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly		365	370	375
Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser				

	380		385		390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr	Leu		
	395	400	405		
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala	Ser		
	410	415	420		
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp	Ala		
	425	430	435		
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr	Ile		
	440	445	450		
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val	Asp		
	455	460	465		
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys	Glu		
	470	475	480		
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr	Glu		
	485	490	495		
Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met	Pro		
	500	505	510		
Arg Ile Ser Lys	Leu Gly Ser Gly Asn	Asp Phe Glu Val Phe	Phe		
	515	520	525		
Gln Arg Leu Gly	Ile Ala Ser Gly Arg	Ala Arg Tyr Thr Lys	Asn		
	530	535	540		
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr	Pro Leu Tyr His Ser	Val		
	545	550	555		
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys	Phe Tyr Asp Pro Met	Phe		
	560	565	570		
Lys Tyr His Leu	Thr Val Ala Gln Val	Arg Gly Gly Met Val	Phe		
	575	580	585		
Glu Leu Ala Asn	Ser Ile Val Leu Pro	Phe Asp Cys Arg Asp	Tyr		
	590	595	600		
Ala Val Val Leu	Arg Lys Tyr Ala Asp	Lys Ile Tyr Ser Ile	Ser		
	605	610	615		
Met Lys His Pro	Gln Glu Met Lys Thr	Tyr Ser Val Ser Phe	Asp		
	620	625	630		
Ser Leu Phe Ser	Ala Val Lys Asn Phe	Thr Glu Ile Ala Ser	Lys		
	635	640	645		
Phe Ser Glu Arg	Leu Gln Asp Phe Asp	Lys Ser Asn Pro Ile	Val		
	650	655	660		
Leu Arg Met Met	Asn Asp Gln Leu Met	Phe Leu Glu Arg Ala	Phe		
	665	670	675		

Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	His	Val
				680					685					690
Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	Phe
				695					700					705
Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp
				710					715					720
Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala
				725					730					735
Ala	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Ser	Glu	Val	Ala
				740					745					750

<210> 619  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 619  
 agatgtgaag gtgcaggtgt gccg 24

<210> 620  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 620  
 gaacatcagc gctcccggta attcc 25

<210> 621  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 621  
 ccagcctttg aatggtacaa aggagagaag aagctcttca atggcc 46

<210> 622  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 622  
 ccaaactcac ccagtgagtg tgagc 25

<400> 624  
cttgttttca ccattgggct aactttgctg ctaggagttc aagccatgcc 50

419